

GenCore version 5.1.3
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OH protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 31 Seconds
(without alignments)

902.922 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 1290 Sequence: MSNRLDGKVAlITGTGLGIG.....NESKFATGSEFVYDGGYTAQ 252

Scoring table: BLOSUM62

GapOpen 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107376 residues

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_03280.*

- 1: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1980.DAT:*
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- 3: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1984.DAT:*
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- 11: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1990.DAT:*
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- 13: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1993.DAT:*
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- 20: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS1/gcadata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1277	99.0	252 18 AAW23407	Lactobacillus brevis
2	1019	79.0	251 18 AWB23409	Lactobacillus kefir
3	456	35.3	254 22 AAB49773	Protein with acetyl
4	450	34.9	254 22 ARB7522	(R)-2-octanoic dehydrogenase
5	400	31.0	258 21 AAY56815	Bacillus D-aramabini
6	369	28.6	272 22 AAU37095	Staphylococcus aur
7	367.5	28.5	261 13 AAR7757	Glucose dehydrogenase
8	364.5	28.3	261 11 AAR04044	Thermostable alcohol(s)
9	364.5	28.3	261 13 AAR24018	Staphylococcus aur
10	354	28.2	251 22 AAB03193	E. megaterium gluc
11	363.5	28.2	272 21 AAB10740	PS Claim 8; Pages 24-26; 34PP; German.

ALIGNMENTS

RESULT 1
ID: AAV23407 standard; Protein; 252 AA.
XX
AC: AAV23407;
XX
DT: 27-MAR-1998 (first entry).

XX
DE: Lactobacillus brevis alcohol dehydrogenase.
XX
KW: Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
XX
OS: Lactobacillus brevis.
XX
PN: EP96914-A2.
XX
PD: 24-SEP-1997.
XX
PF: 20-MAR-1997; 97EP-0104814.
XX
PR: 21-MAR-1996; 96DB-4010984.

XX
PA: (BOEFL) BOEHRINGER MANNHEIM GMBH.
XX
PI: Hummel W, Riebel B;
XX
DR: WPF; 1997-459831/43.
N-PSDB: AAT73132.
XX
PT: Lactobacillus brevis alcohol dehydrogenase - useful for production
of optically active alcohol(s).
XX
PS: Claim 8; Pages 24-26; 34PP; German.

CC The present sequence is a Lactobacillus brevis alcohol dehydrogenase, which retains at least 95% of its activity after 30 minutes at 20-60 degrees C and can be purified to a specific activity of at least 400 U/mg. The enzyme can be used to produce (R)-alcohols by enantioselective reduction of ketones of formula CC R₁-CO-R₂, where R₁ and R₂ = hydrogen (sic) or 1-20C alkyl, alkenyl, aryl or arylene (sic) optionally substituted by halogen, NO₂, OH or 1-20C alkoxy, an optionally substituted 1-10C alkylene group, which is substituted by saturated, unsaturated or aromatic nitrogen, oxygen or sulphur heterocycles, or may be an optionally substituted polycondensed saturated and/or aromatic group (sic) in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol of formula R₁-CHOH-R₂ in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours.

SQ Sequence 252 AA;

Query Match 99.0%; Score 1277; DB 18; Length 252;

Best Local Similarity 99.1%; Pred. No. 6.5e-116; Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSNRDGKVIAITGGTIGLIAITKVEGSAKWMITDSDYGERAKSAKSQGTPDQIQPF	60
Db	1	MSNRDGKVIAITGGTIGLIAITKVEGSAKWMITDSDYGERAKSAKSQGTPDQIQPF	60
Qy	61	QHDSSDEDGTKLFDATETRFGPVSTLVNAGIAVNKSVETTAEWKRLLAVNLGDYFF	120
Db	61	QHDSSDEDGTKLFDATETRFGPVSTLVNAGIAVNKSVETTAEWKRLLAVNLGDYFF	120
Qy	121	GTRLGQMRNKIGASIMSSTEGFVGDPSLGAYNAASKGAVIMSKSAALCALKQD	180
Db	121	GTRLGQMRNKIGASIMSSTEGFVGDPSLGAYNAASKGAVIMSKSAALCALKQD	180
Qy	181	VRVNTVHPGYIKTPVADDLPGAAERAMSQT KTPMHTGPNDIAYICVLAESNEFSKPATG	240
Db	181	VRVNTVHPGYIKTPVADDLPGAAERAMSQT KTPMHTGPNDIAYICVLAESNEFSKPATG	240
Qy	241	SEFVVDGGYTAQ	252
Db	241	SEFVVDGGYTAQ	252

RESULT 2
AAW23409
ID AAW23409 standard; Protein; 251 AA.
XX
AC AAW23409;
XX
DT 27-MAR-1998 (first entry)
DE Lactobacillus kefir alcohol dehydrogenase.
KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
XX
OS Lactobacillus kefir.
XX
FH Key Location/Qualifiers
FT Misc-difference 46 /note= "not defined in specification"
FT Misc-difference 47 /note= "not defined in specification"
FT Misc-difference 48 /note= "not defined in specification"
FT Misc-difference 49 /note= "not defined in specification"
FT Misc-difference 50 /note= "not defined in specification"
FT Misc-difference 51 /note= "not defined in specification"
FT Misc-difference 52 /note= "not defined in specification"
FT Misc-difference 53 /note= "not defined in specification"

PN EP796914-A2.
XX
PD 24-SEP-1997.
XX
PF 20-MAR-1997; 97EP-0104814.
XX
PR 21-MAR-1996; 96DE-41010984.
XX
PA (BOEFL) BOEHRINGER MANNHEIM GMBH.
PI Hummel W, Riebel B;
XX
DR WPI; 1997-459831/43.

XX
PT Lactobacillus kefir alcohol dehydrogenase - useful for production of optically active alcohol(s)
XX
PS Example 8; Pages 28-30; 34PP; German.
XX
CC The present Lactobacillus kefir alcohol dehydrogenase (ADH) was used in the isolation of a L. brevis ADH, which retains at least 95% of its activity after 30 minutes at 20-60 degrees C and can be purified to a specific activity of at least 400 U/mg. The enzyme can be used to produce (R)-alcohols by enantioselective reduction of ketones of formula R₁-CO-R₂, where R₁ and R₂ = hydrogen (sic) or 1-20C alkyl, alkenyl, aryl or arylene (sic) optionally substituted by halogen, NO₂, OH or 1-20C alkoxy, an optionally substituted 1-10C alkylene group, which is substituted by saturated, unsaturated or aromatic nitrogen, oxygen or sulphur heterocycles, or may be an optionally substituted polycondensed saturated and/or aromatic group" (sic) in the presence of the

CC following characteristics:
 CC (1) produces ketones by oxidizing alcohol using beta-NAD as a
 CC co-enzyme; and produces alcohols by reducing ketones using beta-NADH
 CC as a co-enzyme; and
 CC (2) preferentially oxidizes the optical isomer (R)-2-octanol; and
 CC reduces 4-haloacetoacetate ester to produce (S)-4-halo-3-
 CC hydroxybutyrate ester.
 CC (S)-4-halo-3-hydroxybutyrate esters are useful as intermediates
 CC for HMG-CoA reductase inhibitors or D-carnitine. (R)-propoxybenzene
 CC derivatives are particularly useful as intermediates for optical
 CC isomers of ofloxane ((S)-(-)-9-fluoro-3-methyl-10-(4-methyl-1-
 CC piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4) benzoquinu-
 CC 6-carboxylic acid).

XX Sequence 254 AA;

Query Match 34.9%; Score 450; DB 22; Length 254;
 Best Local Similarity 39.0%; Pred. No. 1.6e-35; Gaps 5;

Matches 101; Conservative 46; Mismatches 100; Indels 12; Gaps

5; Pred. No. 1.6e-35; Gaps 5;

Db 1 MSYNPHNKVAVVTGALSGTGLSVAKKFLQGAKTYTISDGEKKYHETVALKAQNLT 59

Qy 1 MSNRDGKVYIITGGTGLGICLAIATKFEVGAKYMTD-----RHSDVGEKAQKVGT 54

Db 2 DNLLHVQADSKEEPNKKLSETIATEFGIDIVCANAGIGKFAPTHETPDWKKVIAVN 119

Qy 2 55 DQIQPFQHDSSDEGWTKLFDATAKEAFGVYSTLVNAGIAVANKSVEETTAEWKLAIN 114

Db 3 60 DNLHVQADSKEEPNKKLSETIATEFGIDIVCANAGIGKFAPTHETPDWKKVIAVN 119

Qy 3 115 LDGVFFGTRIGIORMKNKGLAGAIIINMSSTEGVGDPSLAYNASKAVRIMSKSAALDC 174

Db 4 120 LNGVFLLDKAINTYWLEKSRPGVTVNMGSYHSFVAAPGLAHYGAKGKYLQQTPLAEY 179

Qy 4 175 ALKDGVRYNTVHPGYIKTPVLVDGABEAMSORTKT-PMGHIGEPNDIAYCIVYLASNEK 236

Db 5 180 A--SHGIRVNSVNGYIISPLIDEVP--KERLDKLVSILPIGRIGRPEEVADAFLCSQ 235

Qy 5 234 ESKPATGSEFFVVDGGYTAQ 252

Db 6 236 EATFPINGVSLPVDPDGYTAQ 254

RESULT 5 AAY56815 standard; Protein: 258 AA.

XX ID AAY56815 standard; Protein: 258 AA.

AC AAY56815;

XX DT 31-MAR-2000 (first entry)

XX DE Bacillus sp.

XX KW D-arabinitol dehydrogenase; clinical diagnosis; mycosis.

OS Bacillus sp.

XX PN JP11332569-A.

XX PR 21-MAR-2000; 2000US-191078P.

XX PR 23-MAY-2000; 2000US-206848P.

XX PR 26-MAY-2000; 2000US-20727P.

XX PR 23-OCT-2000; 2000US-242578P.

XX PR 27-NOV-2000; 2000US-251625P.

XX PR 22-DEC-2000; 2000US-257931P.

XX PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KJ, Zyskind JW, Wall D, Travick JD, Carr GJ;

XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70;

XX DR N-PSDB; AAS54954.

XX PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

PT claim 1; Page 10-11; 14pp; Japanese

PS

XX following characteristics:
 CC (1) produces ketones by oxidizing alcohol using beta-NAD as a
 CC co-enzyme; and produces alcohols by reducing ketones using beta-NADH
 CC as a co-enzyme; and
 CC (2) preferentially oxidizes the optical isomer (R)-2-octanol; and
 CC reduces 4-haloacetoacetate ester to produce (S)-4-halo-3-
 CC hydroxybutyrate ester.
 CC (S)-4-halo-3-hydroxybutyrate esters are useful as intermediates
 CC for HMG-CoA reductase inhibitors or D-carnitine. (R)-propoxybenzene
 CC derivatives are particularly useful as intermediates for optical
 CC isomers of ofloxane ((S)-(-)-9-fluoro-3-methyl-10-(4-methyl-1-
 CC piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4) benzoquinu-
 CC 6-carboxylic acid).

XX Sequence 258 AA;

Query Match 31.0%; Score 400; DB 21; Length 258;
 Best Local Similarity 39.4%; Pred. No. 1.2e-30; Mismatches 101; Indels 12; Gaps 7;

Db 4 RLDRGKVAITITGGTGLGICLAIATKFEVGAKYMTIDRHSVDGKEKA---KSVGTPDQIQFF 60

Db 8 RLDRGRTIVTGAGMGLGRANALRQAGSHIVIADIRADEAQEAQNTECSRGCV-EATVV 65

Qy 61 QHDSSDEDGWTKLFDATAKEAFGVYSTLVNAGIAVANKSVEETTAEWKLAVNLGVPP 120

Db 66 QTDVTDQAQEALIIRQEEYGRDLVLYNNAGATVHKDRAEELPYETWNVANYNLNSVPL 125

Qy 121 GTRLGIIQRMRNKGLGASITINMSSTEG-FVGDPDS-LGAYNASKGAVRIMSKSAALDCALRD 178

Db 126 MSKAAGKVMIRQKG-SIINISMSSGLIVNTPOQAOAYNWSKACVIMLKTSLASBWA--P 182

Qy 179 YDVVRNTVHPGYIKTPVLVDD--LPGAAEEMSORTKTPMGHIGEPNDIAYCIVYLASNEK 236

Db 183 HGVRNTIAGYGMTRKLTEPYFAAGGEMIDKWLAMTPMGRGPVHELGIAVTLASDASS 242

Qy 237 FATGSEFVVDGGYT 250

Db 243 FATGCFVFTIDGGYT 256

RESULT 6 AAU37095

ID AAU37095 standard; Protein: 272 AA.

XX AC AAU37095;

XX DT 14-FEB-2002 (first entry)

XX DE Staphylococcus aureus cellular proliferation protein #1265.

XX KW Antisense; prokaryotic cellular proliferation protein;

XX KW antibiotic; antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX DT 27-SEP-2001.

XX XX 21-MAR-2001; 2001WO-US09180.

XX DE Staphylococcus aureus cellular proliferation protein #1265.

XX KW Antisense; prokaryotic cellular proliferation protein;

XX KW antibiotic; antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX DT 14-FEB-2002 (first entry)

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XX KW Antisense; prokaryotic cellular proliferation protein;

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XX KW antibiotic; antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

Example 3; Seq ID No 12680; 51pp; English.

PS FT Misc-difference 43
 XX FT /label= Asp, Glu
 CC FT Misc-difference 79
 CC FT /label= Ala, Ser
 CC FT Misc-difference 95
 CC FT /label= Leu, Met

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

XX SQ Sequence 272 AA:

Query Match 28.6%; Score 369; DB 22; Length 272;
 Best Local Similarity 35.8%; Pred. No. 1.3e-17; Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

Oy 4 RLDGKVAILITGGTGLIGLAIATKVEEAGKVMITDRHSVDGEKAAKSVGTQDQIQRFQHD 63
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 3 RLENKVAVVIGASTGGQASIALAQEAGTVLAVDIAEVSTYDKISNGDRAKAYVD 62
 Qy 64 SSEDGWTKLFDATEKAFGPYSTLYNNAGI-AVNKSVEETTAEWKRLLAVNLGDVFFG 121
 |||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 63 IASEQOIDNPASEIREQFGHVDFLNNAAGR-IHEYPTDVKMNVDRGTFLM 121
 Oy 122 TRLGFIORMKNGLGSIIINNSIEGPVGDPDSLGAYNASKAVRIMSKSAALDCALKDYD 181
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 122 TKGMLPLMOMTK-GGSIVNTSSFSFGQAADLYRSQYNAAKGVINPTKSLIAEYG-RD-GI 177
 Qy 182 RVNTVHPGYIKTPLYDLPGEEL---AMSORTIKTPMGHIGEPNDIAYICVYLASNE 234
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 178 RANATAPGTETPLVPLKLTGTSDEREGKAFRNQRWMTPLGRPEEVGKLVVFLASDE 237
 Qy 235 SKFATGSEFVYDGGYT 251
 |||:|||:
 Db 238 SSFIRCTETIRIDGGYMA 254
 Qy 239 KDFGSEFVYDGGYT 251
 |||:|||:
 Db 237 SYVTGTTLFADGGMT 251

RESULT 7
 PAR27757
 ID AAR27757 standard; protein; 261 AA.
 XX AC AAR04044
 XX DT 02-MAR-1993 (first entry)
 XX DE Glucose dehydrogenase.
 XX KW GDH; mutant; recombinant; mass production; tetramer; thermostable.
 XX OS Bacillus megaterium.
 XX PH Key Location/Qualifiers
 PT Misc-difference 96
 PT Misc-difference /note= "site of Glu->Val or Lys mutation"
 PT Misc-difference 252
 PT Misc-difference /note= "site of Glu->Leu mutation"
 PT Misc-difference 253
 PT Misc-difference /note= "site of Tyr->Glu mutation"
 PT Misc-difference 22
 PT /label= Ser, Ala

FT Misc-difference 43
 FT /label= Asp, Glu
 FT Misc-difference 79
 FT /label= Ala, Ser
 FT Misc-difference 95
 FT /label= Leu, Met

XX PD 14-SEP-1992.
 XX PR 13-FEB-1991; 91JP-0106927.
 XX PR 13-FEB-1991; 91JP-0106927.
 XX PA (AMAN) AMANO PHARM KK.
 XX DR WPI; 1992-354684/43.
 XX PS Claim 1; Page 8; 12pp; Japanese.

XX CC The glucose dehydrogenase enzyme is encoded by a recombinant DNA clone from *Bacillus megaterium*. The DNA sequence may be mutated by site directed mutagenesis to introduce mutations to the protein sequence (see feature table). The DNA may be used to transform *E. coli* cells, and transformants may be cultured to mass produce GDH. The mutant GDH is not influenced by ion strength , exists as a tetramer and is thermostable.
 XX SQ Sequence 261 AA;

Query Match 28.5%; Score 367.5; DB 13; Length 261;
 Best Local Similarity 33.3%; Pred. No. 1.7e-7; Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

Oy 1 MSNRLDGKVAILITGGTGLIGLAIATKVEEAGKVMITDRHSVDGEKA---KSYGTPDQ 56
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 MYKDLGKVVVITGSSTGLGXMAIRFATEAKVYVNRSEKEANSVLEPIKKVG-GE 58
 Qy 57 IQFFQHDSSEDGWTKLFDATEKAFGPYSTLYNNAGI-AVNKSVEETTAEWKRLLAVNL 116
 |||:|||:|||:|||:|||:|||:|||:
 Db 59 AIAVKGDTVYESDVINVQSZIKEFGKLDWMINNAGXENPVSSHMSLSDNKVIDTNLT 118
 Qy 117 GVFGETRLGFIORMKNGLGSIIINNSIEGPVGDPDSLGAYNASKAVRIMSKSAALDCAL 176
 |||:|||:|||:|||:|||:|||:
 Db 119 GAFLGSREAKYFVENDIKGTVINRSSVHEKPTPLFVHYAAASKGGMKLMTETLALEYAP 178
 Qy 177 KDYDVRNTVHPGYIKTPMGHIGEPNDIAYICVYLASNE 235
 |||:|||:|||:|||:
 Db 179 K-GIRVNNIGPAINTPINAEKFADPQRADVSMIPMGYIGEDEIAAVAAWLASSEA 236
 Qy 236 KFATGSEFVYDGGYT 250
 |||:|||:
 Db 237 SYVTGTTLFADGGMT 251

RESULT 8
 AAR04044
 ID AAR04044 standard; protein; 261 AA.
 XX AC AAR04044;
 XX DT 02-MAR-1993 (first entry)
 XX DE Glucose dehydrogenase.
 XX KW GDH; vector; *E. coli*; enzyme; assay; food.
 XX

OS Bacillus megaterium.
 XX Thermostable; increased heat stability; GDH.
 FH XX
 Key Location/Qualifiers
 Misc-difference 22
 PT /label= SER, ALA
 FT
 Misc-difference 43
 FT /label= ASP, GLU
 FT Misc-difference 79
 FT /label= ALA, SER
 FT Misc-difference 95
 FT /label= LEU, MET
 PN JP02072878-A.
 XX
 PD 13-MAR-1990.
 XX
 PP 06-SEP-1988; 88JP-0223343.
 PR 06-SEP-1988; 88JP-0223343.
 PA (AMAN) AMANO PHARM KK.
 XX
 DR WPI; 1990-12104/16.
 PT Glucose dehydrogenase prodn. from Bacillus megaterium - by culturing recombinant DNA-contg. transformants in nutrient culture medium, used in food industry
 XX
 PS Claim 1; 12pp; Japanese.
 XX
 CC DNA encoding glucose dehydrogenase (GDH) derived from B. megaterium encodes the amino acid sequence below. The DNA may be integrated into a vector for replication in E. coli. A large amt. of GDH may be produced at low cost. The GDH is used in clinical laboratory tests in the food industry in enzymic assays for glucose determination.
 XX
 SQ Sequence 261 AA:
 Query Match 28.3%; Score 364.5; DB 11; Length 261;
 Best Local Similarity 33.3%; Pred. No. 3.4e-27;
 Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;
 QY 1 MSNRLDKVAILITGGTGIGLIAKTVVEGAKVMTDRHSVDGERAA---KSVGTPDQ 56
 Db 1 MYKDLERKVWVITGGTSSNLGKMMAIRPAEKVLYKVVNYRSKEEXANSVLEEKVKVKG--GE 58
 Qy 57 TQFFQHSSDDEGWTKLFDATDEKAFGPVSTLVNNAGTAVNKSVEENTTAERKLJAVNL 116
 Db 59 AFAVKGDVTESDVINLVQSKXKEFGDVMINNAGENPVSHEMSLDNKNVIDNLT 118
 Qy 117 GYFFGTRLGIGORMKNGKGLGASTINMMSIEGGTYGDPISGAYNASKGAVRIMSKSAALDCAL 176
 Db 119 GAFGLSREAKYKFVENDIKGTVNMSSVHEK1PWPFLVHASKGGMKLMTEETALEYAP 178
 Qy 177 KDYDVRNTNTVPGYIKTP-LVDDLPGAEAMNSQRTPTPMGIGEPNDIAYTCYLNASNES 235
 Db 179 K-GIRVNNICGGAINTPINAEKFADPQERADSMIPMGIGEPEBIAAAWLASSEA 236
 Qy 236 KFATGSEFVVDDGYT 250
 Db 237 SKVTGTTLFADGGM 251
 SQ Sequence 261 AA:
 RESULT 9
 ID AAR24018 Standard; Protein; 261 AA.
 XX
 AC AAR24018;
 XX
 DT 27-NOV-1992 (first entry)
 XX
 DE Thermostable glucose dehydrogenase from Bacillus megaterium.
 .
 Query Match 28.3%; Score 364.5; DB 13; Length 261;
 Best Local Similarity 33.3%; Pred. No. 3.4e-27;
 Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;
 Qy 1 MSNRDQKVAITGGTLLGIGLIAKTVVEGAKVMTDRHSVDGERAA---KSVGTPDQ 56
 Db 1 MYKDLERKVWVITGGTSSNLGKMMAIRPAEKVLYKVVNYRSKEEXANSVLEEKVKVKG--GE 58
 Qy 57 IQFFQHSSDDEGWTKLFDATDEKAFGPVSTLVNNAGTAVNKSVEENTTAERKLJAVNL 116

CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is used in the
 CC construction of fusion proteins as described in the method of the
 CC invention.

XX Sequence 272 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 272;
 Best Local Similarity 31.5%; Pred. No. 4.5e-27;
 Matches 51; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
 CC

Qy	1 MSNRDGVKVAIRGKTLGILAIATKFVEEGAKYMT-----DRHSDVGEKAAKSY 51
Db	1 MYTDLKDVKVITGGTGTGILAIATKFVEEGAKYMT-----DRHSDVGEKAAKSY 51
Qy	52 GTPDQIQQFHQSDDGWTMKTFLDEDATEKAAGPVSILVNNNGIAVNSVEETTAERKLL 111
Db	61 -----IVGDTVKEEDVNLVOTAIKEEFTGLDYMNNAGVENPVPSHELSLDWNWKV 113
Qy	112 AVNLQGVFFTRIGLQRMNKGLASILINNSSIEFVGDSLGAIVNSKAVRIMSKSA 171
Db	114 DTNLTGAFLGSREREALKYFENDIIGNVNINNSVHEIMPWPLFVHYAASKGMKLMTELA 173
Qy	172 LDCALKDYDVRNVPHPGYTKTPL-VDDLPGAAEMSQRKTPMCHIGENDIAYICVYL 230
Db	174 LEYARK--GTRVNNGPGMNTPINAEKPADPEORADVESMIPMGYIGKPEEEAVAAAPL 231
Qy	231 ASNEKFATGSEFYVDDGGY 250
Db	232 ASSQASVYTGTITLEADGGMT 251

RESULT 12
 AAB10741 ID AAB10741 standard; Protein: 340 AA.
 XX AC AAB10741;
 XX DT 26-JAN-2001 (first entry)
 XX DE H. ghilianii/B. megaterium fusion protein Tridegin/GlcDH.
 XX KW Glucose dehydrogenase; GlcDH; fusion protein; detection; tridegin.
 OS Heamentaria ghilianii.
 OS Bacillus megaterium.

XX Key Location/Qualifiers
 FT 1..68
 Protein "Tridegin protein"
 FT 69..340 /note= "Tridegin protein"
 FT /note= "GlcDH"
 XX PN WO200409039-A2.
 XX PD 24-AUG-2000.
 XX PF 08-FEB-2000; 2000WO-EP00978.
 XX PR 19-FEB-1999; 99DE-1006920.
 XX PA (MERC) MERCK PATENT GMBH.
 XX PD 29-SEP-1988.
 XX PI Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
 XX DR WPI; 2000-558290/51.
 XX N-PSDB; AAA97949.
 XX PA (AMAN) AMANO PHARM KK.

PT PT quick detection of foreign proteins by gel electrophoresis -
 XX Disclosure; Page 59-60; 63pp; German.

CC This invention describes a novel recombinant fusion protein (A)
 CC comprising at least a first and a second amino acid sequence,
 CC characterized in that the first sequence has the biological activity of
 CC a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector
 CC protein (in a detection system) for any type of recombinant
 CC protein/polypeptide in a fusion protein. Glucose dehydrogenase can be
 CC used to detect protein-protein interactions, where it corresponds to a
 CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents a
 CC fusion protein constructed from the H. ghilianii tridegin protein and the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is described in the
 CC method of the invention.

XX SQ Sequence 340 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 340;
 Best Local Similarity 31.5%; Pred. No. 6.1e-27;
 Matches 51; Mismatches 108; Indels 19; Gaps 4;
 CC

Qy	1 MSNRDGVKVAIRGKTLGILAIATKFVEEGAKYMT-----DRHSDVGEKAAKSY 51
Db	69 MYTDLKDVKVITGGTGTGILAIATKFVEEGAKYMT-----DRHSDVGEKAAKSY 51
Qy	52 GTPDQIQQFHQSDDGWTMKTFLDEDATEKAAGPVSILVNNNGIAVNSVEETTAERKLL 111
Db	129 -----IVGDTVKEEDVNLVOTAIKEEFTGLDYMNNAGVENPVPSHELSLDWNWKV 181
Qy	112 AVNLQGVFFTRIGLQRMNKGLASILINNSSIEFVGDSLGAIVNSKAVRIMSKSA 171
Db	182 DTNLTGAFLGSREREALKYFENDIIGNVNINNSVHEIMPWPLFVHYAASKGMKLMTELA 173
Qy	172 LDCALKDYDVRNVPHPGYTKTPL-VDDLPGAAEMSQRKTPMCHIGENDIAYICVYL 230
Db	192 LDCAKDYDVRNVPHPGYTKTPL-VDDLPGAAEMSQRKTPMCHIGENDIAYICVYL 230
Qy	242 LEYARK--GTRVNNGPGMNTPINAEKPADPEORADVESMIPMGYIGKPEEEAVAAPL 299
Db	300 ASSQASVYTGTITLEADGGMT 319

RESULT 13
 AAR03846 ID AAR03846 standard; protein: 261 AA.
 XX AC AAR03846;
 XX DT 09-AUG-1990 (first entry)
 XX DE Modified glucose dehydrogenase; Bacillus megaterium; heat stability;
 XX KW Glucose dehydrogenase; Bacillus megaterium; heat stability;
 XX Glucose assay; ss.
 XX OS Bacillus megaterium.
 XX PN DE3931716-A.
 XX PD 29-SEP-1988.
 XX PI Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
 XX PR 22-SEP-1989; 89DE-3931716.
 XX DR 22-SEP-1988; 88JP-0237699.
 XX PA (AMAN) AMANO PHARM KK.

XX XX (AMAN) AMANO PHARM KK.
 PI XX PA
 XX XX
 DR XX DR; 1992-354681/43.
 XX DR N-PSDB; AAQ9486.
 PT PT New NAD affinity glucose dehydrogenase - obtnd. from Bacillus
 PR megaterium
 XX XX
 PS Disclosure; Page 5; 8pp; Japanese.
 XX
 CC The Bacillus megaterium derived NAD affinity glucose dehydrogenase
 CC may be prep. recombinantly by inserting its gene into a vector and
 CC using this to transform E. coli. The enzyme may be used in a kit to
 CC determine the amt. of glucose in a sample.
 XX
 SQ Sequence 261 AA;
 Query Match 27.9%; Score 359.5; DB 13; Length 261;
 Best Local Similarity 31.9%; Pred. No. 1e-26;
 Matches 83; Conservative 48; Mismatches 110; Indels 19; Gaps 4;
 Qy 1 MSNRLDGKVAITGGTIGLIAATKEVEGAKVMTI-----DRHSDYGEKAASKV 51
 Db 1 MYTDLKPKVVVTGGSGLGRAMAVRQEAKVNTYNNBEALAKKEYEAGQQAI 60
 Qy 52 GTPDQIOFFQHDSSDEGWTKLFDATEKAFGPVSTLNNAGIAVNKSVEETTAEWKL 111
 Db 61 -----IVQGDYTKKEEDVNVLYQATAKEFGTLDMVNNAGVNPVSHELSLDNNNKVI 113
 Qy 112 AVNLQGYFQFGTRGIQMKNGLGASJNMSSTEGFTGDPGJAYNSRGAVRIMSSAA 171
 Db 114 DTNLTGFLGSREAKYFVNIDKGVNIINMSSVHEMPWPLFHYAASKGMKXMTTLA 173
 Qy 172 LDCALKDQYDVRNTVHPGYIKTPL-VDDLPGAEEAMSORTKPMGHIGEPNDIAYCIVYL 230
 Db 174 LEYAPK-GIRNNIGGAMNTPINAEKFADPVERADEVSMIPMGYIGKPEEEVAAYAFL 231
 Qy 231 ASNESKPATGSEFVVDGGYT 250
 Db 232 ASSEASVTGITLEFADGGM 251
 RESULT 15
 AAP80590
 ID AAP80590 standard; protein; 261 AA.
 XX AC AAP80590:
 XX DT 14-SEP-1990 (first entry)
 XX DE Sequence of glucose dehydrogenase (GD) from Bacillus megaterium as
 DE encoded on plasmid pJH11.
 XX KW Bacillus megaterium; non-pathogenic; glucose dehydrogenase;
 KW Plasmid PSA77 (DSM 4054P);
 KW Plasmid PSA24 (DSM 4053P); B. megaterium strain M1296/pSA677 (DSM 4050P);
 KW B. megaterium strain M1296/PSAG2 (DSM 4048); high protein yields;
 KW B. megaterium strain M1296/PSAC4 (DSM 4049); plasmid pJH11.
 XX OS Bacillus megaterium.
 XX PD 12-OCT-1988.
 XX PF 28-MAR-1988; 88EP-0104953.
 XX PN EP285949-A.
 XX DT 13-FEB-1991; 91JP-0187085.
 PR 14-SEP-1992; 87DE-3711883.
 XX PA (MERCK) MERCK PATENT GMBH.
 XX PI Ebeling W, Heilmann HJ, Meinhardt F;

XX WPI; 1988-287162/41.
 DR N-PSDB; AAN81184.
 XX
 PT Genetic control unit for *Bacillus megaterium*
 PT contg. specified promoter sequence
 XX
 PS : Fig 5; 22pp; German.

XX The patent claims new genetic control units which contain at least one promoter region and at least one terminator region, where the region contg. the promoter region is represented by the DNA sequence in AAN81182. The region contg. the terminator region is represented by the DNA sequence in AAN81183. Also claimed are plasmids contg. the promoter region in AAN81182. The region contg. the terminator region is represented by the DNA sequence in AAN81183. Also claimed are plasmids contg. the promoter and *Bacillus megaterium* strains transformed with such plasmids. *B. megaterium* strains contg. structural genes under control of the promoter region produce high yields of the protein encoded by the structural gene, e.g. glucose dehydrogenase (GD) or chlorophenicol acetyltransferase (CAT). Unlike *E. coli*, *B. megaterium* is non-pathogenic and can be used, e.g., in the foodstuffs and water industries. Specifically claimed plasmids are PSA677 (DSM 4055P), contg. DNA coding for GD, PSA62 (DSM 4054P), contg. DNA coding for GD and PSA4 (DSM 4053P), contg. DNA coding for CAT, specifically claimed *B. megaterium* strains are M1296/PSA677 (DSM 4050), M1296/PSA677 (DSM 4048) and M1296/PSA4 (DSM 4049).

XX Sequence 261 AA:

Query	Match	Score	Length
Qy	1 MSNRLDGKVAVITGGTLLGGLAATKEYEGAKYMIT-----DRHSIDGEKAAKSV	358.5	261;
Db	1 MYTDLKDVKVVTGTTGGSTGLGRGNAVRGQEAEAKVINYNNPEEALDKKEYEAGQAI	109;	
Qy	52 GTPDQIQFFQHDSSDEGRTKLFDATEKAQGPYSTLYNNAGIAVNKSWEETTAERKLL	111	
Db	61 -----IVQGDYTKEEKDVNLVQTAIKEFGTLDVMINAGVNPVPSHELSLDNWNKVI	113	
Qy	112 AVNLDGYFEGTRGIORMKNGKLGASILNMSSLEGFYGDPISLGAYNSKGAVRIMSAA	171	
Db	114 DTNTTGAFGSRPAIKYVENDIKGNVINMASSYHEMPWPLVHYASKGGKLMLTEFLA	173	
Qy	172 LOCALKDYDVRVNTVHPGKTKL-VDDLPGABAMSORTKPMGHIGEPNDIAYICVYL	230	
Db	174 LEVAPK--GIRVNTIGPGAMMTPINAEKFADPEQRADVESIMPMSGYIGKPEEEVAAIL	231	
Qy	231 ASNESKFKATGSSEFVVDGSGYT	250	
Db	232 ASSQASVTVGITLEADGGM	251	

Search completed: October 30, 2002, 15:47:05
 Job time : 34 secs

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 : Search time 32 Seconds
(without alignments)

874.706 Million cell updates/sec

Title: US-09-910-033A2

Perfect score: 252

Sequence: 1 MSNRDGKVALLTGGTLGIC.....NESKFATGSEFVVDGGYTAQ 252

Scoring table: OLIGO GapOp 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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RESULT 1
AAW23407

ID AAW23407 standard; Protein: 252 AA.
XX
AC AAW23407;
XX
DT 27-MAR-1998 (first entry)
XX
DE Lactobacillus brevis alcohol dehydrogenase.
XX
KW Alcohol dehydrogenase; production; (R)-alcohol;
XX
OS Lactobacillus brevis.
XX
PN EP796914-A2.
XX
PD 24-SEP-1997.
XX
PF 20-MAR-1997; 97EP-0104814.
XX
PR 21-MAR-1996; 96DE-4010984.
XX
PA (BOEFL) BOEHRINGER MANNHEIM GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WIT: 1997-45983143.
DR NPSDB; AAT73132.
XX
PT Lactobacillus brevis alcohol dehydrogenase - useful for production
of optically active alcohol(s)
XX
PS Claim 8; Pages 24-26; 34pp; German.
XX

Novel human diagno
Peptide #8053 encod
Human bone marrow
Propionibacterium
S. spinosa protein
Protein with acetyl
(R)-2-octanol dehy
ORFL5 protein inv
C glutamic prote
Corynebacterium
Arabidopsis thalial
Arabidopsis thalial
A. thaliana enviro
Arabidopsis thalial
Human liver carbon
Tomato nicotinamin
Maize Ts2 sequence
Arabidopsis thalial
Arabidopsis thalial
Sequence of amino
Arabidopsis thalial
Novel human diagno
Human proton trans
S. clava antimicro
S. clava antimicro
E. coli AMP gene S
Peptide #7686 encod
Human brain expres
Human bone marrow
Peptide #7869 encod
S. pneumoniae 3'-ox
Amino acid sequenc
S. epidermidis ope
Human ORFX ORF1177
S. epidermidis ope

ALIGNMENTS

Result No.	Query	Match	Length	DB ID	Description
1	179	71.0	252	18 AAW23407	Lactobacillus brev
2	47	18.7	251	18 AAW23409	Lactobacillus kefi
3	36	14.3	50	20 AAY30523	L. brevis ADH N-te
4	36	14.3	50	20 AAY33419	L. brevis wild typ
5	28	11.1	50	20 AAY33424	L. brevis ADH pept
6	27	10.7	50	20 AAY33420	L. brevis ADH pept
7	27	10.7	50	20 AAY33421	L. brevis ADH pept
8	27	10.7	50	20 AAY33422	L. brevis ADH pept
9	27	10.7	50	20 AAY33423	L. brevis ADH pept
10	25	9.9	38	18 AAW23408	Lactobacillus kefi
11	20	7.9	34	20 AAY33413	L. brevis NADP-dep

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	179	71.0	252	18 AAW23407	Lactobacillus brev
2	47	18.7	251	18 AAW23409	Lactobacillus kefi
3	36	14.3	50	20 AAY30523	L. brevis ADH N-te
4	36	14.3	50	20 AAY33419	L. brevis wild typ
5	28	11.1	50	20 AAY33424	L. brevis ADH pept
6	27	10.7	50	20 AAY33420	L. brevis ADH pept
7	27	10.7	50	20 AAY33421	L. brevis ADH pept
8	27	10.7	50	20 AAY33422	L. brevis ADH pept
9	27	10.7	50	20 AAY33423	L. brevis ADH pept
10	25	9.9	38	18 AAW23408	Lactobacillus kefi
11	20	7.9	34	20 AAY33413	L. brevis NADP-dep

CC The present sequence is a Lactobacillus brevis alcohol
 CC dehydrogenase, which retains at least 95% of its activity after 30
 CC minutes at 20-60 degrees C and can be purified to a specific
 CC activity of at least 400 U/mg. The enzyme can be used to produce
 CC (R)-alcohols by enantioselective reduction of ketones of formula
 CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
 CC aryl or arylene (sic) optionally substituted by halogen, NO₂, OH
 CC or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group,
 CC which is substituted by saturated, unsaturated or aromatic
 CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
 CC substituted polycaprolactam saturated and/or aromatic group" (sic) in
 CC the presence of the enzyme or cells containing it at 20-60 degrees
 CC C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol
 CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
 CC containing it at 20-60 degrees C for 0.25-3 hours.

XX Sequence 252 AA;

Query Match 71.0%; Score 179; DB 18; Length 252;

Best Local Similarity 100.0%; Pred. No. 3.6e-170;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	39	RHSDVGEKAKSQVTPDPQTQFQDSSDEGWTKLFDATKAFGPVSTLNNAGIAVNKS	98
Db	39	RHSDVGEKAKSQVTPDPQTQFQDSSDEGWTKLFDATKAFGPVSTLNNAGIAVNKS	98
Qy	99	VEETTAENRKLLAVNLDDGWFTRGLGIORMKNGLGASTINNSIEGVGDP SIGAYNA	158
Db	99	VEETTAENRKLLAVNLDDGWFTRGLGIORMKNGLGASTINNSIEGVGDP SIGAYNA	158
Qy	159	SKGAVRIMSKSAALDCALKDYDVRNTVHPGYIKTPPLDLPGAEAMSQRTRKPMGHI	217
Db	159	SKGAVRIMSKSAALDCALKDYDVRNTVHPGYIKTPPLDLPGAEAMSQRTRKPMGHI	217

RESULT 2

ID AAW73409 standard; Protein: 251 AA.
 XX
 AC AAW73409;
 XX
 DT 27-MAR-1998 (first entry)

XX DE Lactobacillus kefir alcohol dehydrogenase.

XX KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
 XX OS Lactobacillus kefir.
 XX KEY Location/Qualifiers
 FH Misc-difference 46 /note= "not defined in specification"
 FT Misc-difference 47 /note= "not defined in specification"
 FH Misc-difference 48 /note= "not defined in specification"
 FT Misc-difference 49 /note= "not defined in specification"
 FT Misc-difference 50 /note= "not defined in specification"
 FT Misc-difference 51 /note= "not defined in specification"
 FT Misc-difference 52 /note= "not defined in specification"
 FT Misc-difference 53 /note= "not defined in specification"
 FT Misc-difference 54 /note= "not defined in specification"
 FT Misc-difference 55 /note= "not defined in specification"
 FT Misc-difference 56 /note= "not defined in specification"
 FT Misc-difference 57 /note= "not defined in specification"

PN EP796914-A2.

XX

PD 24-SEP-1997.

XX

PP 20-MAR-1997; 97EP-0104814.
 XX PR 21-MAR-1996; 96DE-4010984.
 XX PA (BOEFL) BOHRINGER MANNHEIM GMBH.

XX PI Hummel W, Riebel B;

XX DR WPI; 1997-459831/43.

XX PT Lactobacillus brevis alcohol dehydrogenase - useful for production
 PT of optically active alcohol(s)
 XX PS Example 8; Pages 28-30; 34pp; German.
 XX
 CC The present Lactobacillus kefir alcohol dehydrogenase (ADH) was
 CC used in the isolation of a L. brevis ADH, which retains at least
 CC 95% of its activity after 30 minutes at 20-60 degrees C and can be
 CC purified to a specific activity of at least 400 U/mg. The enzyme
 CC can be used to produce (R)-alcohols by enantioselective reduction
 CC of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic)
 CC or 1-20C alkyl, alkenyl, aryl or arylene (sic) optionally
 CC substituted by halogen, NO₂, OH or 1-20C alkoxy, "an optionally
 CC saturated, unsaturated or aromatic nitrogen, oxygen or sulphur
 CC heterocycles, or may be an optionally substituted polycaprolactam
 CC saturated and/or aromatic group" (sic) in the presence of the
 CC enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours,
 CC or (S)-alcohols by incubating a racemic alcohol of formula
 CC R1-CHOH-R2 in the presence of the enzyme or cells containing it at
 CC 20-60 degrees C for 0.25-3 hours.
 XX SQ Sequence 251 AA;18.7%; Score 47; DB 18; Length 251;
 Query Match

Best Local Similarity	100.0%	Pred.	No. 1.6e-38;	XX	L. brevis wild-type ADH peptide fragment.
Matches	47;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	DE	DE
Qy	153	LGYNASKAVRIMSKSALDCALKDVRVNTVHPGVIKTPLYDDL	199	XX	KW
Db	152	LGYNASKAVRIMSKSALDCALKDVRVNTVHPGVIKTPLYDDL	198	KW	NADPH-dependent dehydrogenase; NADH-specificity; coenzyme docking region; R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
				XX	KW
				OS	R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
				XX	Lactobacillus brevis.
				PN	W09947684-A2.
RESULT 3				XX	
ID	AAV30523	standard; peptide:	50 AA.	XX	
XX	AAV30523;			PD	23-SEP-1999.
AC				XX	18-MAR-1999;
DF	03-DEC-1999	(first entry)		PF	99WO-DE00848.
XX				XX	
DE	L. brevis ADH N-terminal peptide fragment.			PR	19-MAR-1998;
XX				XX	98DE-1012004.
KW	ADH; alcohol dehydrogenase; NADH specificity; coenzyme docking region;			PA	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
KW	NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;			PA	
KW	R-hydroxy-compound; keto-compound; S-hydroxy-compound.			PI	Hummel W, Riebel B;
XX				XX	
OS	Lactobacillus brevis.			DR	WPI; 1999-571842/48.
XX				XX	
PN	W09947684-A2.			PT	Improving NADH-specificity of NADPH-dependent dehydrogenases by recombinant microbial techniques -
XX				PT	
PD	23-SEP-1999.			PS	Claim 10; Page 30; 35pp; German.
XX	99WO-DE00848.			XX	
PF	18-MAR-1999;			CC	This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology.
PR	19-MAR-1998;	99DE-1012004.		CC	The improved dehydrogenases can be used for stereo-selective extraction of R-hydroxy-compounds through enzymatic reduction of the corresponding keto-compound. They can also be used for stereo-selective extraction of S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of the R-hydroxy-compound. The dehydrogenases have improved temperature and pH optimums and improved stability. This sequence represents a wild-type Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX				CC	
PS	Sequence: Page 2; 35pp; German.			SQ	Sequence 50 AA.
XX				Query Match	Score 36; DB 20; Length 50;
CC	This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the basicity of the coenzyme docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology.			Best Local Similarity	100.0%; Pred. No. 3.5e-28;
CC	The improved dehydrogenase can be used for stereo-selective extraction of R-hydroxy-compounds through enzymatic reduction of the corresponding keto-compound. They can also be used for stereo-selective extraction of S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of the R-hydroxy-compound. The dehydrogenases have improved temperature and pH optimums and improved stability. This sequence represents the N-terminal fragment of Lactobacillus brevis alcohol dehydrogenase (ADH).			Mismatches	0; Indels 0; Gaps 0;
CC				QY	2 SNRLDGKVAITGGTLGIGLAIATKFVEEGAKVMT 37
CC				Db	1 SNRLDGKVAITGGTLGIGLAIATKFVEEGAKVMT 36
CC				RESULT 5	
CC				ID	AAV33424
CC				AC	AAV33424 standard; peptide: 50 AA.
CC				XX	
CC				XX	
CC				DT	03-DEC-1999 (first entry)
CC				XX	
CC				DE	L. brevis ADH peptide fragment mutant 2/2.
CC				XX	
CC				XX	
CC				XX	
CC				XX	
CC				XX	
CC				OS	
CC				OS	
CC				OS	
CC				OS	
CC				SYNTHETIC	
CC				XX	
CC				PN	W09947684-A2.
CC				XX	
CC				PD	23-SEP-1999.
CC				XX	
CC				PF	18-MAR-1999; 99WO-DE00848.
RESULT 4					
ID	AAV33419				
XX	standard; peptide:	50 AA.			
AC	AAV33419;				
XX					
DT	03-DEC-1999 (first entry)				

XX 19-MAR-1998; 98DE-1012004.
 CC PR
 CC XX
 CC PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 CC XX
 CC PI Hummel W, Riebel B;
 CC XX
 CC DR WPI; 1999-571842/48.
 CC XX
 CC PT Improving NADH-specificity of NADPH-dependent dehydrogenases by recombinant microbial techniques -
 CC XX
 PS Claim 10; Page 30; 35pp; German.
 XX SQ Sequence 50 AA;
 CC This invention describes a novel method for improving NADH-specificity of preferred NADH-dependent dehydrogenase. The method comprises a reduction in the the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology. The improved dehydrogenase can be used for stereo-selective extraction of R-hydroxy-compounds through enzymatic reduction of the corresponding keto-compound. They can also be used for stereo-selective extraction of S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of the R-hydroxy-compound. The dehydrogenases have improved temperature and pH optimums and improved stability. This sequence represents a mutant Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
 XX SQ Sequence 50 AA;
 CC This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology. The improved dehydrogenase can be used for stereo-selective extraction of R-hydroxy-compounds through enzymatic reduction of the corresponding keto-compound. They can also be used for stereo-selective extraction of S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of the R-hydroxy-compound. The dehydrogenases have improved temperature and pH optimums and improved stability. This sequence represents a mutant Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
 XX SQ Sequence 50 AA;
 Query Match 11.1%; Score 28; DB 20; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.3e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 IITGGTIGGLATAATKFVEGAKVMT 38
 Db 10 IITGGTIGGLATAATKFVEGAKVMT 37
 RESULT 6
 AAY33420 ID AAY33420 standard; peptide; 50 AA.
 XX AC AAY33420;
 XX DT 03-DEC-1999 (first entry)
 XX L. brevis ADH peptide fragment mutant 1.
 XX DE ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region; NADPH-dependent dehydrogenase; stereo-selective extraction; racemic; R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
 XX KW Lactobacillus brevis.
 XX OS Synthetic.
 XX PN WO9947684-A2.
 XX PD 23-SEP-1999.
 XX PR 18-MAR-1999; 99WO-DE00848.
 XX PR 19-MAR-1998; 98DE-1012004.
 XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX PI Hummel W, Riebel B;
 XX DR WPT; 1999-571842/48.
 XX PN WO9947684-A2.
 XX PD 23-SEP-1999.
 XX PR 18-MAR-1999; 99WO-DE00848.
 XX PR 19-MAR-1998; 98DE-1012004.
 XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX PI Hummel W, Riebel B;
 XX DR WPT; 1999-571842/48.
 XX Improving NADH-specificity of NADPH-dependent dehydrogenases by recombinant microbial techniques -
 XX PS Claim 10; Page 30; 35pp; German.
 CC This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology. The improved dehydrogenase can be used for stereo-selective extraction of R-hydroxy-compounds through enzymatic reduction of the corresponding keto-compound. They can also be used for stereo-selective extraction of S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of the R-hydroxy-compound. The dehydrogenases have improved temperature and pH optimums and improved stability. This sequence represents a mutant Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
 XX SQ Sequence 50 AA;

Query Match	10.7%	Score 27;	DB 20;	Length 50;	XX	03-DEC-1999	(first entry)
Best Local Similarity	100.0%	Pred. No.	3.3e-19;		DT		
Matches	27;	Conservative	0;	Mismatches	0;	Gaps	0;
				Indels	0;		
Qy	11 IITGGTIGIGIAIATFVEGAKVMT 37				XX	L. brevis ADH peptide fragment mutant 2/2.	
Db	10 IITGGTIGIGIAIATFVEGAKVMT 36				DE	ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;	
					XX	NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;	
					KW	R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.	
					XX	Lactobacillus brevis.	
					OS	OS Synthetic.	
RESULT 8					XX		
ID AAY33422	standard; peptide; 50 AA.				XX	W0947684-A2.	
XX					XX		
AC AAY33422;					PD	23-SEP-1999.	
XX					XX	18-MAR-1999;	99WO-DE00848.
DP 03-DEC-1999	(first entry)				XX	19-MAR-1998;	98DE-1012004.
XX					PA	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	
DE L. brevis ADH peptide fragment mutant 2.					XX		
XX ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;					PI	Hummel W, Riebel B;	
XX NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;					XX	WPI; 1999-571842/48.	
XX R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.					XX	Improving NADH-specificity of NADPH-dependent dehydrogenases by recombinant microbial techniques	
OS Lactobacillus brevis.					PS	Claim 10; Page 30; 35pp; German.	
OS Synthetic.					XX	This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology.	
XX W0947684-A2.					CC	The improved dehydrogenase can be used for stereo-selective extraction of CC R-hydroxy-compounds through enzymatic reduction of the corresponding CC keto-compound. They can also be used for stereo-selective extraction of CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of CC the R-hydroxy-compound. The dehydrogenases have improved temperature and CC pH optimums and improved stability. This sequence represents a mutant CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.	
XX WO947684-A2.					XX	Sequence 50 AA;	
XX 23-SEP-1999.					CC	Query Match Score 27; DB 20; Length 50;	
XX PR 18-MAR-1999;	99WO-DE00848.				CC	Best Local Similarity 100.0%; Pred. No. 3.3e-19;	
XX PR 19-MAR-1998;	98DE-1012004.				CC	Matches 0; Mismatches 0; Indels 0; Gaps 0;	
XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.					Qy	11 IITGGTIGIGIAIATFVEGAKVMT 37	
XX PI Hummel W, Riebel B;					Db	10 IITGGTIGIGIAIATFVEGAKVMT 36	
XX DR 1999-571842/48.					RESULT 10		
XX FT Improving NADH-specificity of NADPH-dependent dehydrogenases by recombinant microbial techniques					ID AAW23408		
XX PS Claim 10; Page 30; 35pp; German.					ID AAW23408 standard; peptide; 38 AA.		
XX This invention describes a novel method for improving NADH-specificity of preferred NADPH-dependent dehydrogenase. The method comprises a reduction in the basicity of the coenzyme-docking region of the enzyme through alteration of the relevant amino acid sequence using genetic technology.					XX AC AAW23408;		
CC The improved dehydrogenase can be used for stereo-selective extraction of CC R-hydroxy-compounds through enzymatic reduction of the corresponding CC keto-compound. They can also be used for stereo-selective extraction of CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of CC the R-hydroxy-compound. The dehydrogenases have improved temperature and CC pH optimums and improved stability. This sequence represents a mutant CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.					XX AC AAW23408;		
XX SQ Sequence 50 AA;					XX AC AAW23408;		
XX Query Match Score 27; DB 20; Length 50;					XX AC AAW23408;		
XX Best Local Similarity 100.0%; Pred. No. 3.3e-19;					XX AC AAW23408;		
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					XX AC AAW23408;		
Qy 11 IITGGTIGIGIAIATFVEGAKVMT 37					XX AC AAW23408;		
Db 10 IITGGTIGIGIAIATFVEGAKVMT 36					XX AC AAW23408;		
RESULT 9					XX AC AAW23408;		
RAY33423					XX AC AAW23408;		
ID AAY33423 standard; peptide; 50 AA.					XX AC AAW23408;		
XX AC AAY33423;					XX AC AAW23408;		

DS DR WPI; 2001-639362/73.
DR N-PSDB; AAS71665.
XX
PN New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PP Claim 20: SEQ ID No 37837; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful as sequencing tags
CC for sequencing of the genome. (II) is useful as sequencing tags
CC for sequencing of the genome.
XX
PA (KERJ) FORSCHUNGSENTRUM JUELICH GMBH.
XX
DI Hummel W, Riebel B;
XX
WPI; 1999-571842/48.
XX

CC to restore normal activity of (II) or to treat disease states involving
 CC (III). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (III) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG3377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 86 LYNNAGI 93
 Db 82 LYNNAGI 89

RESULT 13
 ABB40547

ID ABB40547 standard; Peptide; 120 AA.

XX ABB40547;

XX DT 04-FEB-2002 (first entry)

Peptide #8053 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX OS Homo sapiens.
 PN WO200157277-A2.
 XX 09-AUG-2001.
 XX PR 30-JAN-2001; 2001WO-US00669.

XX PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0618408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE') MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX PS Example 4; SEQ ID NO: 34482; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow -

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention.

XX Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 LYNNAGI 94
 Db 87 LYNNAGI 94

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 LYNNAGI 94
 Db 87 LYNNAGI 94

RESULT 14
 ABB4176

ID ABB4176 standard; Protein; 120 AA.

XX ABB4176;

XX AC AM74176;

XX DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 34482.

XX DE Human bone marrow expressed exon; gene expression analysis; probe;

XX KW Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US00668.

XX PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0618408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE') MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX PS Example 4; SEQ ID NO: 34482; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow -

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is a

CC protein encoded by one of the probes of the invention.

XX Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LYNNAGI 94

Db 87 LYNNAGI 94

RESULT 15

AAU55352 AAU55352 standard; Protein; 136 AA.
 XX ID
 XX AAU55352;
 XX AC
 XX XX
 DT 27-FEB-2002 (first entry)
 DE Propionibacterium acnes immunogenic protein #16248.
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes.
 PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PP 20-APR-2001; 2001WO-US12865.
 XX PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR 2001-616774/71.
 XX DR N-PSDB; AA559569.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX PS Example 1; SEQ ID NO 16547; 1069pp; English.
 XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://www.wipo.int/pdb/published_pct_sequences](http://www.wipo.int/pdb/published_pct_sequences).
 XX SQ Sequence 136 AA;
 Query Match 3.2%; Score 8; DB 22; Length 136;
 Best Local Similarity 100.0%; Pred No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 88 VNAGTAV 95
 Qy 111111
 Db 34 VNAGTAV 41
 Db 111111
 Search completed: October 30, 2002, 15:48:00

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OM protein - protein search, using SW model

Run on: October 30, 2002, 15:46:30 ; Search time 19 Seconds
(without alignments)
1274.448 Million cell updates/sec

title: US-09-910-033A-2
perfect score: 252
Sequence: 1 MSNRLDGKVALITGGTIGI.....NESKFATGSEEFVVDGGTAAQ 252
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs; 96089334 residues

Word size : 0

total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	10	4.0	29	2	SI4099	12-alpha-hydroxyst 2-deoxy-D-glucosat hypothetical prote
2	10	4.0	260	2	B81668	probable short cha hypothetical prote
3	9	3.6	250	2	T20258	probable short cha
4	9	3.6	267	2	T11579	hypothetical 1-dehydroglucose 1-dehydro
5	9	3.6	283	2	B81603	short-chain alcoho
6	9	3.6	289	2	D63825	probable short-cha
7	9	3.6	303	2	T46064	hypothetical prote
8	8	3.2	238	2	G81126	hypothetical prote
9	8	3.2	249	2	S47055	probable short-cha
10	8	3.2	251	2	T24180	hypothetical prote
11	8	3.2	251	2	T03564	probable short-cha
12	8	3.2	251	2	AC0103	2-deoxy-D-glucosat 3-oxoacyl-(acyl ca
13	8	3.2	252	2	D83766	hypothetical prote
14	8	3.2	252	2	G72618	hypothetical prote
15	8	3.2	254	2	B87630	short chain dehydr
16	8	3.2	254	2	AD3182	reductase (AL13.82
17	8	3.2	257	2	C93348	short chain dehydr
18	8	3.2	257	2	AD2934	probable short-cha
19	8	3.2	263	2	A98301	dehydrogenase Acu3
20	8	3.2	263	2	AG2982	alcohol dehydrogen
21	8	3.2	272	2	T47354	carbonyl reductase
22	8	3.2	276	2	JCS285	carbonyl reductase
23	8	3.2	277	1	RBDUCB	carbonyl reductase
24	8	3.2	277	2	JCS284	hypothetical prote
25	8	3.2	277	2	T25800	probable Methyldhi
26	8	3.2	307	2	S62472	hypothetical prote
27	8	3.2	335	2	T24540	short-chain alcoho
28	8	3.2	335	2	AG7542	probable amino aci
29	8	3.2	475	2	T00620	

ALIGNMENTS

RESULT 1							
SI4099	12-alpha-hydroxysteroid dehydrogenase - Clostridium sp. (strain C 48-50)	C;Species: Clostridium sp.	A;Variety: strain C 48-50	C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997	C;Accession: SI4099	R;Braun, M.; Lueisdorf, H.; Bueckmann, A.F.	Eur. J. Biochem. 196, 439-450, 1991
							A;Title: 12-alpha-hydroxysteroid dehydrogenase from Clostridium group P, strain C 48-50
							A;Reference number: SI4099; MUID:91177018
							A;Status: Preliminary
							A;Molecule type: protein
							A;Residues: 1-29
Qy	6 DGKVAITGG 15	4.0%	Score 10;	DB 2;	Length 29;	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Similarity 100.0% Pred. No. 0.0054;
Db	4 DGKVAITGG 13						Cross-references: GB:AE005673; PIDN:913425088; NID:GN00148
Qy	6 DGKVAITGG 15	4.0%	Score 10;	DB 2;	Length 29;	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Similarity 100.0% Pred. No. 0.0054;
Db	4 DGKVAITGG 13						Cross-references: GB:AE005673; PIDN:913425088; NID:GN00148

A;Experimental source: cultivar Columbia; BAC clone T18N14.

C;Genetics:

A;Map position: 3

A;Introns: 31/2

A;Note: T18N14.60

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.68; Score 9; DB 2; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GKVATIGG 15

Db 34 GKVATIGG 42

RESULT 8

G33126

probable short-chain dehydrogenase PA4162 [imported] - *Pseudomonas aeruginosa* (strain PA

F) sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: GB33126

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brandom, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337

A;Accession: G83126

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-238 <STO>

A;Cross-references: GB:AE004832; GB:AE004091; NID:99950360; PIDN:AAG07549.1; GSDB:GN001

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA4162

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 238;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LYNNAGTA 94

Db 73 LYNNAGTA 80

RESULT 9

S47055

hypothetical protein 5 - Xanthobacter sp

C;Species: Xanthobacter sp.

C;Accession: S47055

R;Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.

A;Description: Plasmid of xanthobacter Py2 mutants in epoxyalkane degradation; expr

A;Reference number: S47055

A;Accession: S47055

A;Molecule type: DNA

A;Residues: 1-249 <SWA>

A;Cross-references: EMBL:Y79863; NID:g520947; PIDN:CAA56245.1; PID:g520952

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH>

F;5-181/Domain: short-chain alcohol dehydrogenase homology <SDH>

Query Match 3.2%; Score 8; DB 2; Length 249;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LYNNAGTA 94

Db 82 LYNNAGTA 89

RESULT 10

T24180

hypothetical protein R11D1.11 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

R;Steward, C.

C;Accession: T24180

A;Reference number: Z19850

A;Accession: T24180

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-251 <WIL>

A;Cross-references: EMBL:Z75547; PIDN:CAA99897.1; GSDB:GN00023; CESP:R11D1.11

A;Experimental source: clone R11D1

C;Genetics:

A;Gene: CESP:R11D1.11

A;Map Position: 5

A;Introns: 56/3; 157/1; 196/3

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

RESULT 11

T06364

probable short-chain alcohol-dehydrogenase (EC 1.1.1.1.) - tomato (fragment)

C;Species: *Lycopersicon esculentum* (tomato)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C;Accession: T06364

R;Jacobsen, S.E.; Olszewski, N.E.

Planta 198, 78-86, 1996

A;Title: Gibberellins regulate the abundance of RNAs with sequence similarity to pro

A;Reference number: Z15627; MUID:96158488

A;Accession: T06364

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-251 <TAC>

A;Cross-references: EMBL:U21801; NID:g717141; PIDN:AAB00109.1; PID:g717142

A;Experimental source: cultivar Moneymaker

C;Genetics:

A;Gene: GAN3

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; oxidoreductase

RESULT 12

AC0103

2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) [imported] - *Yersinia pestis* (stra

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C;Accession: AC0103

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dongan, C.

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586350

A;Accession: AC0103

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 ; Search time 12 Seconds
(without alignments)
813.111 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 252

Sequence: 1 MSNRILDGVIALITGGTGTGIG.....NESKEFATGSEFFVVDGGYTAQ 252

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs , 38719550 residues

Word size : 0

total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID				Description
		Match	Length	DB	ID	
1	10	4.0	29	1	12AH_CLOSA	P21215 clostridium
2	9	3.6	289	1	YHDE_BACSU	0071575 bacillus su
3	8	3.2	251	1	CBRA_CAEEL	Q21929 caenorhabdi
4	8	3.2	276	1	DHCA_HUMAN	P16152 homo sapien
5	8	3.2	276	1	DHCA_RAT	P47727 rattus norvegicus
6	8	3.2	307	1	YAC2_SCHEO	Q09816 schizosaccharomyces pombe
7	8	3.2	336	1	TS2_MAIZE	P50160 zea mays (m)
8	8	2.8	103	1	NTPG_ENTHR	P3455 enterocecal
9	7	2.8	141	1	HBA_MUSPF	P02423 mustela put
10	7	2.8	141	1	HBA_SPECI	P09420 spermophilus
11	7	2.8	141	1	HBA_SPEPA	P11750 spermophilidae
12	7	2.8	178	1	BDH_BOVIN	Q02337 bos taurus
13	7	2.8	205	1	VATO_HUMAN	Q09437 homo sapien
14	7	2.8	211	1	PCP1_SUPSO	P58201 sulfobulus
15	7	2.8	228	1	PLPA_MEVFO	P55553 methanococcus
16	7	2.8	241	1	BUDC_KLEIE	Q04520 klebsiella
17	7	2.8	241	1	PHBB_RHIME	P50205 rhizobium m
18	7	2.8	241	1	PHBB_ZORA	P23238 zoogloea ra
19	7	2.8	242	1	FABG_HAELIN	P43713 haemophilus
20	7	2.8	242	1	MYFG6_CHICK	Q01795 gallus gallus
21	7	2.8	242	1	PHAB_PARD	P50204 paracoccus
22	7	2.8	244	1	FABG_ECOLI	P25716 escherichia
23	7	2.8	244	1	FABG_SALTY	085141 salmonella
24	7	2.8	244	1	FABG_VIBCH	Q5kqkh7 vibrio cholerae
25	7	2.8	244	1	FABG_VIBHA	P55336 vibrio harveyi
26	7	2.8	245	1	NODG_RHIME	P06234 rhizobium m
27	7	2.8	245	1	NODG_RHIS3	P72332 rhizobium sphaericum
28	7	2.8	246	1	FABG_BACSU	P18331 bacillus su
29	7	2.8	246	1	FABG_THEME	Q9x248 thermotoga
30	7	2.8	246	1	NODG_AZOB	P17611 azospirillum
31	7	2.8	247	1	FABG_MYCTU	Q48930 mycobacteri
32	7	2.8	247	1	PAGL_SYNA3	P73574 synochocystis
33	7	2.8	247	1	YGFP_ECOLI	P52037 escherichia

ALIGNMENTS

RESULT 1	12AH_CLOSA	STANDARD;	PRT;	29 AA.
ID	12AH_CLOSA			
AC	P21215;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	01-AUG-1991 (Rel. 19, Last annotation update)			
DE	12-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.176) (Fragment).			
OS	Clostridium sp. (strain C 48-50).			
OC	Bacteria; Firmicutes; Clostridiaceae; Clostridium.			
OX	NCBI_TaxID=1507;			
RN	[1]			
RP	SEQUENCE.			
RX	MEIDLINE-91177018; PubMed=2007406;			
RA	Braun M., Lünsdorf H., Bueckmann A.F.;			
RT	*12 alpha-hydroxysteroid dehydrogenase from Clostridium group P, strain C 48-50. Production, purification and characterization.;			
RT	EUR. J. Biochem. 196:39-45(1991).			
CC	-I- FUNCTION: CATALYSES THE OXIDATION OF THE 12-ALPHA-HYDROXYL GROUP OF BILE ACIDS, BOTH IN THEIR FREE AND CONJUGATED FORM. ALSO ACTS ON BILE ALCOHOLS.			
CC	-I- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholanate + NADP(+)= 3-alpha,7-alpha-dihydroxy-12-oxo-5-beta-cholanate + NADPH.			
CC	-I- SUBUNIT: HOMOTETRAMER.			
CC	-I- MISCELLANEOUS: THE THERMOSTABILITY OF THE ENZYME IS GREATLY INCREASED DUE TO NADP BINDING.			
DR	PIR: SI4099; SI4099.			
KW	Oxidoreductase; NADP.			
FT	NON_TER	29	Score 10;	DB 1;
SEQ	SEQUENCE	29 AA:	2900 MW;	AB27DB34DB6C8812 CRC64;
Query Match	Best Local Similarity	100.0%	Score 10;	DB 1;
	Mismatches	0;	Pred. No. 0.0022;	Length 29;
	Matches	10;	Conservative	0;
	Indels	0;	Gaps	0;
Qy	6 DGKVATTGG 15			
Db	4 DGKVATTGG 13			

RESULT 2	YHDF_BACSU	STANDARD;	PRT;	289 AA.
ID	YHDF_BACSU			
AC	007575;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DE	Hypothetical oxidoreductase yhdf (EC 1.1.1.140).			
GN	YHDF.			
OS	Bacteria; Firmicutes; Bacillus subtilis.			
OC	Bacillus; Firmicutes; Bacillus/Clostridium group; Bacillus.			
OC	Bacillus/Spaethioccocus group; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			

RN	SEQUENCE FROM N.A.	Db	
RP	Medline=20289759; PubMed=10830953;	86 LYNNAGIA 93	
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Choi D.-K., Soeda E., Park H.-S., Toyota A., Ishii K., Totoki Y., Taudien S., Blechschmidt K., Polley A., Ohki M., Takagi T., Sakaki Y., Patterson D., Menzel U., Delabar J., Kumpf K., Lehmann R., Reichwald K., Kudo J., Schilli Lihab M., Rosenthal A., Schudy A., Zimmermann W., Shintani A., Sasaki T., Shibuya K., Kawasaki K., Asatawa S., Minoshima S., Shimaizu N., Nagamine K., Mitsuyama S., Antonarakis S.E., Schafre M., Schoen O., Desario A., Brandt P., Ramser J., Beck A., Klages S., Hornig S., Rieselselmann L., Dagand E., Wehrmeyer S., Borzdyk K., Gardner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.; RT "The DNA sequence of human chromosome 21.";		
RL	Nature 405:311-319(2000).	RN [7]	
RP	PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.	RN [8]	
RA	Krook M., Ghosh D., Stromberg R., Carlquist M., Joernvall H.; RT "Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-dependent prostaglandin dehydrogenase.";	RN [9]	
RL	Proc. Natl. Acad. Sci. U.S.A. 90:502-506 (1993).	RN [10]	
CC	-1- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL COMPOUNDS INCLUDING THE ANTIDRUG ANTHRACYCLINE ANTIBIOTICS.	RN [11]	
CC	CAN CONVERT PROSTAGLANDIN E2 TO PROSTAGLANDIN F2 ALPHA.	RN [12]	
CC	-1- CATALYTIC ACTIVITY: R-CH(OH)-R' + NADP(+) = R-CO-R' + NADPH.	RN [13]	
CC	-1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9,11,15-trihydroxyprosta-5,13-dienoate + NADP(+) = (5Z,13E)-(15S)-11,15-dihydroxyprosta-5,13-dienoate + NADPH.	RN [14]	
CC	-1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11-alpha,15-dihydroxy-9-	RN [15]	
CC	oxoprost-13-enolate + NADP(+) = (5Z,13E)-11-alpha-hydroxy-9,15-dioxoprost-13-enolate + NADPH.	RN [16]	
CC	-1- SUBCELLULAR LOCATION: MONOMER.	RN [17]	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	RN [18]	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RN [19]	
DR	J04056; AAAS52070.1;	EMBL: X84349; CAA55088.1;	DR
DR	EMBL: M62420; AAA17881.1;	EMBL: X93986; CAA65230.1;	DR
DR	EMBL: AB003151; BAA33498.1;	InterPro: IPR002199; ADH_short.	DR
DR	EMBL: AP000688; BAA89424.1;	PFam: PF00106; adh_short; 1.	DR
DR	EMBL: AP001724; BAA95509.1;	PRINTS: PR00081; GDRDH.	DR
DR	PIR: A31912; RDHUCB.	PROSITE: PS00061; ADH_SHORT; 1.	DR
DR	HSSP: S09013; S09013.	Oxidoreductase; NADP; Acetylation.	KW
DR	INIT_MET 0 0	INIT_MET 0 0	
FT	MOD_RES 1 1	MOD_RES 1 1	ACETYLATION.
FT	NP_BIND 238 238	NP_BIND 238 238	N6-(1-CARBOXYETHYL);
FT	ACT_SITE 9 33	ACT_SITE 9 33	NADP (BY SIMILARITY).
FT	SEQUENCE 193 193	SEQUENCE 193 193	BY SIMILARITY.
SQ	276 AA; 30244 MW; 78E83065F567733 CRC64;	276 AA; 30244 MW; 99B9E77C5E2322AB CRC64;	
Query Match	3.2%	Score 8; DB 1; Length 276;	
Best Local Similarity	100.0%	Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;	
Matches 8; Conservative	0;		
YQ	87 LYNNAGIA 94	87 LYNNAGIA 94	
Db			
Db	86 LYNNAGIA 93	86 LYNNAGIA 93	
RESULT 6			
YAC2_SCIP0			
ID YAC2_SCIP0			
AC Q0816;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Hypothetical 33.9 kDa protein C16C9.02C in chromosome I.			
GN SP16C9.02C			
OS Schizosaccharomyces pombe (Fission yeast).			
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomycetidae;			
OC Schizosaccharomyctaceae;			

CC Schirosaccharonyces.
 CC NCBI_TAXID=4896;
 OC OR
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE PNP/MTAP FAMILY 2 OF PHOSPHORYLASES.

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CC DR EMBL: Z54366; CAA91190_1; -
 DR HSSP: Q13126; JCB0.
 DR InterPro: IPR01369; Mtap_PNP.
 DR Pfam: PF00896; Mtap_PNP; 1.
 DR PROSITE: PS01240; PNP_MTPP-2; 1.
 KW Hypothetical protein; Transferase; Glycosyltransferase.
 SEQUENCE 307 AA: A283285BBD438067 CRC64;

Query Match Score 8; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 GASINMS 142
 Db 192 GASINMS 199

RESULT 7
 ID TS2_MAIZE STANDARD; PRT; 316 AA.
 AC P50160;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Sex determination protein tasselseed 2.
 GN TS2.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv_W22;
 RX MEDLINE=33361991; PubMed=8358795;
 RA DeLong A., Calderon-Urraa A., Dellaporta S.L.;
 RT "Sex determination gene TASSLSEED2 of maize encodes a short-chain alcohol dehydrogenase required for stage-specific floral organ abortion." RT Cell 74:757-768 (1993).
 RL -1- FUNCTION: REQUIRED FOR STAGE-SPECIFIC FLORAL ORGAN ABORTION.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC DR EMBL: L20621; AAC37345_1; -
 DR HSSP; P1992; HDC.
 DR Maizedb; 56963;
 DR InterPro: IPR02198; ADH_short.

DR PF000106; adh_short; 1.
 DR PRINS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; Developmental protein.
 FT NP_BIND 53 93
 FT ACT_SITE 207 207 BY SIMILARITY.
 SQ SEQUENCE 336 AA: 35204 MW: 4E273D6152B0BB99 CRC64;

Query Match Score 8; DB 1; Length 336;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLDGKVAI 11
 Db 52 RLDGKVAI .59

RESULT 8
 ID NTPG_ENTHR STANDARD; PRT; 103 AA.
 AC PA3455;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE V-type sodium ATP synthase subunit G (EC 3.6.3.14) (Na(+)- translocating ATPase subunit G).
 GN NTPG OR NTPQ.
 OS Enterococcus hirae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OC NCBI_TaxID=1354;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 9790;
 RX MEDLINE=34209269; PubMed=8157629;
 RA Takase K., Kakunuma S., Yamato T., Konishi K., Igarashi K., RA Kakunuma Y.;
 RA Solioz M., Davies K.;
 RT *Sequencing and characterization of the ntp gene cluster for vacuolar-type Na(+) translocating ATPase of Enterococcus hirae.*; RT vacuolar-type Na(+) translocating ATPase subunit G.
 RL J. Biol. Chem. 269:11037-11044 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 9790;
 RX MEDLINE=34193617; PubMed=8144530;
 RA Solioz M., Davies K.;
 RT Operon of vacuolar-type Na(+) ATPase of Enterococcus hirae.*;
 RL J. Biol. Chem. 269:9453-9459 (1994).
 CC -1- FUNCTION: INVOLVED IN ATP-DRIVEN SODIUM EXTRUSION.
 CC -1- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.
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 CC DR EMBL: D17462; BAA04274_1; -
 DR EMBL; X76913; CAA54240_1; -
 DR InterPro; IPR002841; Atp-synt_F.
 DR Pfam: PF01990; ATP-synt_F; 1.
 DR PRODOM; PD03611; ATP-synt_F; 1.
 KW Hydrolase; ATP synthase; Hydrogen ion transport.
 SQ SEQUENCE 103 AA: 5F452721633D3960 CRC64;

Query Match Score 7; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTLGIGL 21
 Db 111111
 DR 81 GTLGIGL 87

RESULT 9

HBA_MUSPF	STANDARD;	PRT;	141 AA.
ID P20243;			
DR 01-FEB-1991 (Rel. 17, Created)			
DR 15-DEC-1998 (Rel. 37, Last sequence update)			
RA Hemoglobin alpha-1 and alpha-2 chains.			
DE Mustela putorius furo (Ferret).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae; Mustela.			
NCBI_TaxID=96669;			
RN [1]			
RP			
SEQUENCE.			
MEDLINE=90121748; PubMed=2610931;			
RA Hombrados I., Vidal Y., Rodewald K., Braunitzer G., Neuza J. E.;			
RT "Carnivora: the primary structure of the alpha-chains of ferret (Mustela putorius furo, Mustelidae) hemoglobins.";			
RA Biol. Chem. Hoppe-Seyler 370:1133-1138(1989).			
-1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF ALPHA-1.			
CC PIR: S06138; HAMNIF.			
DR HSSP: P01922; 1BZ0.			
DR InterPro; IPRO002338; Alpha_haem.			
DR InterPro; IPRO00971; Globin.			
DR Pfam; PF00042; globin_1.			
DR PRINTS; PRO0612; ALPHAHAEM.			
DR PROSITE; PS01033; GLOBIN_1.			
RW Hemoglobin transport; Transport; Erythrocyte;			
KW Polymorphism.			
FT METAL	58	58	IRON (HEME DISTAL LIGAND).
FT METAL	87	87	IRON (HEME PROXIMAL LIGAND).
FT VARIANT	15	15	D -> G (IN ALPHA-2 CHAIN).
SQ SEQUENCE	141 AA;	15199 MW;	D0EA19424B09A88E CRC64;

Query Match Score 7; DB 1; Length 141;

Best Local Similarity 100.0%	Pred. No. 11;
Matches 7; Conservative 0;	Mismatches 0;
Indels 0;	Gaps 0;

DR 196 VDDLGKA 202

DB 73 VDDLGKA 79

RESULT 10

HBA_SPECI	STANDARD;	PRT;	141 AA.
ID HBA_SPECI			
AC P09420;			
DR 01-MAR-1989 (Rel. 10, Created)			
DR 01-MAR-1989 (Rel. 10, Last sequence update)			
RA Hemoglobin alpha chain.			
OS Spermophilus citellus (European suslik) (Citellus citellus).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurinae; Spermophilus.			
CC NCBI_TaxID=9997;			
RN [1]			
RP			
SEQUENCE.			
MEDLINE=87128535; PubMed=3814354;			
RA Soskic V., Grulic-Injac B., Braunitzer G.;			
RT "The primary structure of the hemoglobin of the European Souslik (Citellus citellus, Rodentia)." ;			
FT Biol. Chem. Hoppe-Seyler 367:1159-1166(1986).			
FL PIR: A25359; A25359.			
DR HSSP: P01922; 1BZ0.			
DR InterPro; IPRO002338; Alpha_haem.			
DR InterPro; IPRO00971; Globin.			
DR Pfam; PF00042; globin_1.			
DR PRINTS; PRO0612; ALPHAHAEM.			
DR PROSITE; PS01033; GLOBIN_1.			
RW Hemoglobin transport; Transport; Erythrocyte;			
KW Polymorphism.			
FT METAL	58	58	IRON (HEME DISTAL LIGAND).
FT METAL	87	87	IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE	141 AA;	15047 MW;	FF0D9DF6552DF72 CRC64;

Query Match Score 7; DB 1; Length 141;

Best Local Similarity 100.0%	Pred. No. 11;
Matches 7; Conservative 0;	Mismatches 0;
Indels 0;	Gaps 0;

DR 196 VDDLGKA 202

DB 73 VDDLGKA 79

RESULT 12

BDH_BOVIN	STANDARD;	PRT;	178 AA.
ID BDH_BOVIN			
AC Q02337;			
DR 01-OCT-1993 (Rel. 27, Created)			
DT 01-OCT-1993 (Rel. 27, Last sequence update)			
DF 01-OCT-1996 (Rel. 34, Last annotation update)			
RA D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH)			
RT (3'-hydroxybutyrate dehydrogenase) (Fragments).			
FT			
GN			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pechora; Bovidea; Bovidae; Bovine; Bos.			
NCBI_TaxID=9913;			
OX			
RN [1]			

RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=93348395; PubMed=1639787;
RA Marks A.R., McEntyre J.O., Duncan T.M., Erdjument-Bromage H.,
RA Tempst P., Flescher S.;
RT "Molecular cloning and characterization of (R)-3-hydroxybutyrate dehydrogenase from human heart.";
RL J. Biol. Chem. 267:15459-15463(1992).
RN [21]
RP SEQUENCE OF 69-80 AND 127-143.
RC TISSUE=Heart;
RX MEDLINE=86295814; PubMed=35227172;
RA Prasad P.V., Hateri Y.;
RT "Amino acid sequences of two tryptic peptides from D(-)-beta-hydroxybutyrate dehydrogenase radiolabeled at essential carboxyl and sulphydryl groups.";
RL Biochem. Int. 12:941-949(1986).
CC -I - CATALYTIC ACTIVITY: (R)-3-hydroxybutanoate + NAD(+) = acetoacetate + NAD.
CC -I - COFACTOR: REQUIRES PHOSPHATIDYLCHOLINE AS AN ALLOSTERIC ACTIVATOR FOR ENZYMIC ACTIVITY.
CC -I - SUBUNIT: HOMOTETRAMER.
CC -I - SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -I - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
DR PIR: B4245; B42845.
DR HSSP: P14061; I10L.
DR InterPro: IPR02198; ADH_short.
DR PROSITE: PS00061; ADH_SHORT; PARTIAL.
KW Oxidoreductases; NAD; Mitochondrion; Inner membrane.
FT NON_CONS 43 44
FT NON_CONS 80 81
FT NON_CONS 99 100
FT NON_CONS 126 127
FT NON_CONS 164 165
SQ SEQUENCE 178 AA; 19303 MW; 399BF046FAAD6CD5 CRC64;

Query Match Score 2.8%; Best Local Similarity 100.0%; Length 178; Matches 7; Pred. No. 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LYNNAGI 93
Db 47 LYNNAGI 53

RESULT 13
ID VATO_HUMAN STANDARD; PRP; 205 AA.
AC Q99437;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VATO ATP synthase 21 kDa proteolipid subunit (EC 3.6.3.14) (BHTPL).
GN ATP6F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN VATO_TaxID=9606; VATO_ID=11.
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98317536; PubMed=9653649;
RA Nishigori H., Yamada S., Tomura H., Fernald A.A., le Beau M.M., Takeuchi T., Takeeda J.;
RA RT Identification and characterization of the gene encoding a second proton-lipid subunit of human vacuolar H(+)-ATPase (ATP6F).
RN Genomics 50:222-228(1998).
CC -I - FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC

CC -I - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR.
CC -I - TISSUE SPECIFICITY: UBIQUITOUS.
CC -I - SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.

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CC DR EMBL: D89052; BAA13753.1; -.
DR MIM: 603717; -.
DR InterPro: IPR02379; ATPase_C.
DR InterPro: IPR000245; Vac ATPase.
DR Pfam: PF00137; ATP_Synth_C; 2.
DR PRINTS: PRO0122; VACATPASE.
CC DR KW Hydrolase; Hydrogen ion transport; ATP synthesis; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
SQ SEQUENCE 205 AA; 21406 MW; F17C688D068A2785 CRC64;

Query Match Score 2.8%; Best Local Similarity 100.0%; Length 205; Matches 7; Pred. No. 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LGIGIA 23
Db 52 LGIGIA 58

RESULT 14
ID PCP1_SULSO STANDARD; PRT; 211 AA.
AC P58201;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Pyrrolidone-carboxylate Peptidase 1 (EC 3.4.19.3) (5'-oxoprolyl-peptidase 1) (Pyroglutamyl-peptidase I 1) (PGP-I 1).
GN PCP1 OR SS0165.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=2133296; PubMed=11427726;
RA She O., Singh R.K., Confolonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan Weiher C.-Y., Clausen I.G., Curtiss B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heijkamp-de Jong I., Jeffries A.C., Kozares C.J., Medina N., Peng X., Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J., RT The complete genome of the crenarchaeon Sulfolobus solfataricus P2.*.
RN Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC -I - FUNCTION: REMOVES 5'-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID RESIDUES EXCEPT L-PROLINE (BY SIMILARITY).
CC -I - CATALYTIC ACTIVITY: 5'-oxoprolyl-peptide + H(2)O = 5'-oxoproline + peptide.
CC -I - SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -I - SUBCELLULAR LOCATION: Cyttoplasmic (BY similarity).
CC -I - SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15 (THIOL PROTEASE).
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DR EMBL; AE006762; AAK41693.;
 DR InterPro: IPR008016; Peptidase_C15.
 DR Pfam; PF01470; Peptidase_C15; 1.
 DR PRODOM; PD008480; Peptidase_C15; 1.
 DR PROSITE; PS01333; PYRASE_GIU; 1.
 DR PROSITE; PS01334; PYRASE_CYS; 1.
 KW Hydrolase; Thiole protease; Complete proteome.
 FT ACT_STRE 79 79 BY SIMILARITY.
 FT ACT_STRE 142 142 BY SIMILARITY.
 FT ACT_STRE 164 164 BY SIMILARITY.
 SQ SEQUENCE 211 AA; 23680 MW; 84416BE3CB745AB4 CRC64;

Query Match 2.88; Score 7; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 16 TUGIGLA 22
 |||||
 Db 64 TUGIGLA 70

RESULT 15
 F1PFA_METVO
 ID F1PFA_METVO STANDARD PRT; 228 AA.
 AC P35553;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Fibrillarin-like pre-rRNA processing protein.
 GN F1PFA OR RPPA.
 OS Methanococcus voltae.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus;
 OX NCBI_TAXID=2188;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC STRAIN=DSM 1537 /
 RX MEDLINE=94193565; PubMed=8144483;
 RA Agha Aniru K.;
 RT "Fibrillarin-like proteins in the domain Archaea.";
 RL J. Bacteriol. 176:2124-2127(1994).
 CC -I- FUNCTION: MAY BE INVOLVED IN PRE-RRNA PROCESSING.
 CC -I- SIMILARITY: BELONGS TO THE FIBRILLARIN FAMILY.
 CC

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DR EMBL; X73988; CA052166.1;
 DR PIR; S34646; S34646.
 DR HSSP; Q58108; IFPRN.
 DR InterPro: IPR00692; Fibrillarin.
 DR Pfam; PF01269; Fibrillarin_1.
 DR PRINTS; PR00052; FIBRILLARIN.
 DR PRODOM; PD004637; Fibrillarin_1.
 DR PROSITE; PS00566; FIBRILLARIN_1.
 KW RNA processing; RNA-binding.
 SQ SEQUENCE 228 AA; 25618 MW; 0AB2418DE0E324CF CRC64;

Query Match 2.88; Score 7; DB 1; Length 220;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 134 LGASII 140
 |||||

Db 57 LGASII 63

Search completed: October 30, 2002, 15:47:21
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - Protein search, using SW model

Run on: October 30, 2002, 15:46:05 ; Search time 27 Seconds
(without alignments)

Scoring table: OLIGO
GapOp 60.0 , GapExt 60.0

Title: US-09-910-033a-2

Perfect score: 252

Sequence: 1 MSNRLDGKVALITGGTIGIG.....NESKFATGSEFVVDGGYTAQ 252

Post-processing: Listing first 45 summaries

Database : SPTREMBL_19.*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database : SPTREMBL_19.*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodobacter:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archeap:*

1: sp_archaea:*

RESULT 2

Q93RM0	PRELIMINARY;	PRT;	247 AA.
ID Q93RM0;			
AC Q93RM0;			
STRAIN=NCIMB 9871;			
RA Iwaki H., Hasegawa Y., Teraoka M., Tokuyama T., Lau P.C.;			
RT "Identification and Characterization of Cyclohexanol Metabolic Genes from Acinetobacter sp. NCIMB 9871.";			
RT EMBL: AB026668; BAB61742; MW: AB0DA7904DE726B3 CRC64;			
DR			
SQ			

Query Match 4.0%; Score 10; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;

Qy 186 VHPGKIKPL 195
 Db 185 VHPGKIKPL 194

RESULT 3

Q9FTE0	PRELIMINARY;	PRT;	251 AA.
ID Q9FTE0;			
AC			
STRAIN=NCIMB 9870;			
RA Iwaki H., Hasegawa Y., Teraoka M., Tokuyama T., Lau P.C.;			
RT "Identification and Characterization of Cyclohexanol Metabolic Genes from Acinetobacter sp. NCIMB 9870.";			
RT EMBL: AB026668; BAB61742; MW: AB0DA7904DE726B3 CRC64;			
DR			
SQ			

Query Match 4.0%; Score 10; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;

Qy 186 VHPGKIKPL 195
 Db 185 VHPGKIKPL 194

RESULT 5

Q9A326	PRELIMINARY;	PRT;	260 AA.
ID Q9A326;			
AC Q9A326;			
STRAIN=ATCC 19089;			
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson R.C., Stephens C., Phadikar S., Gwinn M.L., Haft D.H., Kolonay J.P., Dodson R.J., Durkin A.S., Craven M.B., Smits J., Berry K., Utterback T., Tran K., Wolf A., Yamatievean J., Ermolaeva M., White O., Salzberg S.L., Ventter J.C., Shapiro L., Fraser C.M.;			
RT "Complete genome sequence of Caulobacter crescentus.";			
DR Proc. Natl. Acad. Sci. U.S.A. 98:1136-1141(2001).			
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.			
DR AE005999; AAC25342.1; -.			
DR HSSP: P19992; 1HDC.			
DR TIGR: CC3380; -.			
DR InterPro: IPR02198; ADH_short.			
DR Pfam: PF00106; adh_short; 1.			
DR PRINTS: PRO0080; SDRFAMILY.			
KW Complete proteome; Oxidoreductase; UNKNOWN_1.			
SQ SEQUENCE 260 AA; P19992 MW: 26992 MW;			
Query Match 4.0%; Score 10; DB 16; Length 260; Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;			
Qy 111 LAVNLDGVFF 120 Db 116 LAVNLDGVFF 125			

RESULT 6

Q9A366	PRELIMINARY;	PRT;	250 AA.
ID Q9A366;			
AC Q9A366;			
STRAIN=SP119;			
RA MEDLINE=20398154; PubMed=10940012;			
RT Chang Q., Thomas S.M., Kostichka K., Valentine J.R., Nagarajan V.;"Genetic analysis of a gene cluster for cyclohexanol oxidation in acinetobacter sp. strain SE19 by in vitro transposition.";			
RT IBL: 182:1474-151(2000).			
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.			
DR EMBL: AF282240; AAC10046.1; -.			
DR HSSP: P19992; 1HDC.			
DR InterPro: IPR002198; ADH_short.			
DR PRINTS: PR00080; SDRFAMILY.			
KW Oxidoreductase.			
SQ SEQUENCE 251 AA; B5BA48055997D5D CRC64;			
Query Match 4.0%; Score 10; DB 2; Length 251; Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;			
Qy 186 VHGGYIKPL 195 Db 189 VHGGYIKPL 198			

RESULT 4

DR Intercepto; IPR00198; ADH_short.
 DR PF00106; adh_short; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 250 AA; 27060 MW; 95A2C768163B82CE CRC64;
 Query Match 3.6%; Score 9; DB 5; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 LYNNAGTAV 95
 DB 85 LYNNAGTAV 93

RESULT 6
 ID P93697 PRELIMINARY; PRT; 267 AA.
 AC P93697;
 DT 01-MAY-1997 (TRMBLrel. 03, Created)
 DT 01-MAY-1997 (TRMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE CPRD12 PROTEIN.
 OS Vigna unguiculata (Cowpea).
 OC Spermato phyta; Streptophyta; Embryophyta; Tracheophyta;
 eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 OX NCBI_TaxID=3917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Iuchi S., Yamaguchi-Shinozaki K., Urao T., Shinozaki K.;
 RT "Characterization of two cDNAs for novel drought-inducible genes in
 the highly drought-tolerant cowpea.";
 RL J. Plant Res. 109:415-424(1996).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL: D88121; BAA13541.1; -.
 DR HSSP; P19992; 1INDC.
 DR Intercepto; IPR00198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PRO0080; SDRFAMILY.
 DR PROSITE; PS0061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 267 AA; 28484 MW; 8C4A48A2E9F41B64 CRC64;
 Query Match 3.6%; Score 9; DB 10; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GKVAITGG 15
 DB 16 GKVAITGG 24

RESULT 7
 ID Q9A4H3 PRELIMINARY; PRT; 283 AA.
 AC Q9A4H3;
 DT 01-JUN-2001 (TRMBLrel. 17, Created)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE OXIDOREDUCTASE, SHORT-CHAIN DEHYDROGENASE/REDUCTASE FAMILY.
 GN CC2864.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 NCBI_TaxID=69394;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisner J., Heidelberg J.F., Alley M.R.K., Ohta N., Madlock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., ElY B.,

RA Debay R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vaithayanathan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Ventre J.C., Shapiro L., Fraser C.M.;
 RT *Complete genome sequence of Caulobacter crescentus.*;
 RL PROC. NATL. ACAD. SCI. U.S.A. 98:4136-4141 (2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL; AE005951; AAK24825.1; -.
 DR HSSP; P14061; 1FDW.
 DR TIGR; CC2861; -.
 DR InterPro; IPR002198; ADH_short.
 DR PRINTS; PRO0080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 283 AA; 29715 MW; 6913D8BE681F2D46 CRC64;
 Query Match 3.6%; Score 9; DB 16; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 87 LVNNAGTAV 95
 DR 84 LVNNAGTAV 92
 RN [1]
 RP SEQUENCE FROM N.A.
 ID Q9SCU0 PRELIMINARY; PRT; 303 AA.
 AC Q9SCU0;
 DT 01-MAY-2000 (TRMBLrel. 13, Created)
 DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
 DE SHORT-CHAIN ALCOHOL DEHYDROGENASE-LIKE PROTEIN.
 GN T18N14.60.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; core eudicots; Rosidae;
 OC Spermatophytia; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Delisey M., Berger C., Cooke R., Grellet F., Laudie M., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X., Quettier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL; AL132968; CAB63154.1; -.
 DR HSSP; P19992; 1HDC.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PRO0080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 303 AA; 32151 MW; DC1BD28DABE38DD6 CRC64;
 Query Match 3.6%; Score 9; DB 10; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GKVAITGG 15
 DR 34 GKVAITGG 42
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisner J., Heidelberg J.F., Alley M.R.K., Ohta N., Madlock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., ElY B.,
 RA RESULT 9
 Q9TSA9 PRELIMINARY;
 AC Q9TSA9; PRT; 65 AA.

RESULT 13

Q56841	ID	056841;	PRELIMINARY;	PRT;	249 AA.	
AC	Q56841;					
DT	01-NOV-1996	(TREMBLrel. 01, Created)				
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)				
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)				
DE	ORE5 PROTEIN.					
GN	Xanthobacter sp.					
OS	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Hyphomicrobium group; Xanthobacter.					
OC	NCBI_TAXID=35809;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-N.Y;					
RX	Swaving J., Weijters C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.; "Complementation of Xanthobacter Py2 mutants in epoxylane DNA fragment: expression and nucleotide sequence of the complementing DNA fragment." Microbiology 141:477-484 (1995).					
RT	-1 - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY					
RT	EMBL; X79863; CAA56245.1; -.					
RT	HSSP; P19992; 1HDC.					
RT	InterPro: IPR002198; ADH_short.					
PFAM:	PF00106; adh_short; 1.					
RL	PRINTS; PR00080; SDRFAMILY.					
DR	PROSTATE; PS00061; ADH_SHORT; UNKNOWN_1.					
DR	Oxidoreductase.					
KW	SEQUENCE 249 AA; 24940 MW; B5E0B82C1D8D9782 CRC64;					
SQ						

Query Match Score 3.2%; Best Local Similarity 100.0%; Pred. No. 12; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LYNNAGIA 94
Db 82 LYNNAGIA 89

RESULT 14

Q937L4	ID	0937L4;	PRELIMINARY;	PRT;	250 AA.	
AC	Q937L4;					
DT	01-DEC-2001	(TREMBLrel. 19, Created)				
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)				
DE	CYCLOHEXANOL DEHYDROGENASE (EC 1.1.1.1).					
GN	CPNB.					
OS	Comamonas testosteronei (Pseudomonas testosteronei).					
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.					
OX	NCBL_TAXID=385;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN-NCIMB 9872;					
RA	van Beilen J.B., Fritzsche U., Seeger M., Smits T.H.M., Witholt B.; "Cloning of Baeyer-Villiger monooxygenases from Comamonas, Xanthobacter and Rhodococcus via PCR with highly degenerate primers." Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.					
RT	DR AJ418060; CADD10799.1; -.					
RT	Oxidoreductase.					
KW	SEQUENCE 250 AA; 26626 MW; 7C42C3CBAEBBB85BE CRC64;					
SQ						

Query Match Score 3.2%; Best Local Similarity 100.0%; Pred. No. 12; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 VWDGGYTA 251
Db 242 VWDGGYTA 249

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 05 : (without alignments)
1210.726 Million cell updates/sec

Title: US-09-910-033A-2
perfect score: 1290
Sequence: 1 MSRLDGKVAITGGTIG... NESKFATCSEFVYDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.1*

1: PIR1;*

2: PIR2;*

3: PIR3;*

4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	36.4	261	B07279	hypothetical prote
2	464.5	36.0	260	H70758	probable fabG pro
3	400.5	31.6	255	1 S10707	20beta-hydroxyster
4	400.5	31.0	255	1 S39737	glucose 1-dehydro
5	393	30.5	254	2 S48129	3 (or 17)beta-hydro
6	383	30.3	249	2 S70755	hypothetical prote
7	380	29.7	256	2 E72427	oxidoreductase, sh
8	374.5	29.5	247	2 E70740	probable fabG pro
9	372.5	29.0	248	2 F69868	glucose 1-dehydrog
10	371.5	28.9	253	2 B95284	probable [impaired
11	365.5	28.8	261	2 J50385	glucose 1-dehydrog
12	370.5	28.7	261	2 A3528	acetoin dehydrogen
13	368	28.5	253	2 B86737	probable dehydroge
14	367	28.4	258	2 C70885	hypothetical prote
15	366	28.3	272	2 A99950	3-oxoacyl-(acyl) ca
16	365.5	28.3	246	2 H72219	glucose 1-dehydrog
17	365.5	28.3	263	2 S01227	dehydrogenase Atu5
18	364.5	28.3	255	2 D70635	probable [impaired
19	363.5	28.2	261	1 S00812	glucose 1-dehydrog
20	363	28.1	262	2 S02299	probable short cha
21	359	27.8	254	2 AD3182	hypothetical prote
22	358.5	27.8	261	2 D69629	3-oxoacyl-(acyl) ca
23	357.5	27.7	251	2 AI3185	3-oxoacyl-(acyl) ca
24	357.5	27.7	258	2 D95284	glucose 1-dehydrog
25	357.5	27.7	261	2 I40225	probable short cha
26	357.5	27.7	271	2 AC0157	hypothetical prote
27	357	27.7	296	2 EB7260	3-oxoacyl-(acyl) ca
28	356.5	27.6	248	2 H98258	3-oxoacyl-(acyl) ca
29	356.5	27.6	248	2 AI3025	3-oxoacyl-(acyl) ca

RESULTS

RESULT 1

B07279

hypothetical protein CC0246 [Imported] - Caulobacter crescentus

C; Species: Caulobacter crescentus

C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C; Accession: E87279

R; Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Debay, R.M.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kc n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A; Title: Complete Genome Sequence of Caulobacter crescentus.

A; Reference number: A87249; PMID:21173698; PMID:11259647

A; Accession: E87279

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-261 <STOP>

A; Cross-references: GB:AE005673; NID:q13421377; PIDN:AAK22233.1; GSPDB:GN00148

ALIGNMENTS

Query Match Score 36.4%; Best Local Similarity 40.7%; Matches 107;保守性 46; Mismatches 90; Indels 20; Gaps 6;

Qy 2 SNRLDGKVAITGGTIGIGLAIATRVEEGAKVMTDRHSVGEKAKSVGTDPDQIQ--- 58
Db 5 TGRVAGKAFITGGAGGLGAAGRMIAKEGAKVAL---ADINLACAGAQAVA--DEINAAH 58
Qy 59 -----FQHQSSDEDTGWTKLFDATEKAFGPVSTLYNAGTAVNKSVEETTAENWRKLLA 112
Db 59 GAGTAAFAFELDTQEQWIDVLEKATAAMGGLSVLYNNAGGDDGPIESLDFGLNKVMS 118
Qy 113 VNLDGFVFGRFLGIORMKNGLGAISIIMNSIEFGVGDPSLGAYNAKGAVRIMSKSAAL 172
Db 119 VNDVSYFLGKHALTHMRAGPQ---SINLNSIAGLTIANGSPAYNAKAYWLLSINIAL 177
Qy 173 DCALKDYDVNTVHPGYTKTPLYDPLP---GAERAMSORTK-TPMHGICRPNDIAYICV 228
Db 178 YCAKURLDIKRSNSTHPTFIDPLQGFSARFGKEEAFAKLARQVPLGRICEPTDIAVNL 237
Qy 229 YLASNESKFKATGSEFVVDGGYTA 251
Db 238 YLASDESKEWTGAEALKVGGTSA 260

RESULT 2

H70758

probable fabG3 protein - Mycobacterium tuberculosis (strain H37RV)

C; Species: Mycobacterium tuberculosis

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C; Accession: H70758

R-Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	Qy 123 RLQFQRMKKGASLINTSSIEGVGDPSPSGYNAVRIMSKRVALDCAKRDYDVR 182 Db 120 KTVIPAMKDAG-GGSIVNASSAAGLMGLATSYGASWVGRLSKLAEE-LGTIRIR 176
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	Qy 183 VNTVHPGYITKPLVDDLPGAEEAMSORTKTPMGHIG-EPNDIAVTCVYLASNESKFATGS 241
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	Db 177 VNSVHPGNTYTPMTAE-TGIROGEGNYPNTPMGRVGEPETAGVYKLSPDTSSYTGTA 235
A;Reference number: A70500; MUID:9825987	Qy 242 EFVFDGGTT 250 Db 236 ELAVDGNT 244
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	Qy 244 EFVFDGGTT 250 Db 236 ELAVDGNT 244
A;Cross references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98414.1; PID:g3261591	RESULT 4 S39737 giucose 1-dehydrogenase homolog ywfd - <i>Bacillus subtilis</i> N;Alternative names: protein Ipa-82d N;Contains: probable dehydrogenase (EC 1.1.1.-) C;Species: <i>Bacillus subtilis</i> C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: S39737; E70555 R;Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Jones, A.; Rapoport, G.; Danchin, A. Mol. Microbiol. 10, 371-384, 1993 A;Title: <i>Bacillus subtilis</i> genome project: cloning and sequencing of the 97 kb region A;Reference number: S39655; MUID:95020537 A;Accession: S39737 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-255 <GLA> A;Cross-references: EMBL:X73124; NID:9413023; PIDN:CAA51638.1; PID:9414006 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993 R;Kunst, F.; Ogasawara, N.; Mozer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Capriano, V.; Carter, N.M.; C.; Erlich, S.D.; Emerson, P.R.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997 A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gaiech, J.; Harwood, C.R.; Hanaut, A.; Hilbert, H.; Hollsper, S.; Hosono, S.; Hullo, Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardir, A; Authors: Lauber, J.; Liu, S.M.; Lee, A.; Levine, A.; Liu, S.M.; Masuda, S.; Ma Y., M.; Ogawa, K.; Ogivara, A.; Oudege, B.; Par, S.H.; Parro, V.; Pohl, T.M.; Portet Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadeie, Y.; Sato, T.; Scan A; Authors: Schleicher, S.; Schoeter, R.; Terpstra, P.; Toononi, A.; Uchii, S.; Akeuchil, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Toononi, A.; Uchii, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshihikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> A;Accession number: A6580; MUID:98040433 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-255 <KUNP> A;Cross-references: GB:Z99123; GB:AL009126; PIDN:92636240; PIDN:CAA15799.1; PID:g2636 A;Experimental source: strain 168 C;Genetics: A;Gene: ywfd C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology C;Keywords: NAD; oxidoreductase F;8-183/Domain: short-chain alcohol dehydrogenase homology <SADH> RESULT 3 S10707 241 SERFVDDGTYA 251 Db 230 AEEFVDDGTV 240
C;Species: Streptomyces exfoliatus	Query Match 31.6%; Score 407.5; DB 1; Length 255; Best Local Similarity 39.0%; Pred. No. 3.8e-25; Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
C;Accession: S10707	Query Match 31.6%; Score 407.5; DB 1; Length 255; Best Local Similarity 39.0%; Pred. No. 3.8e-25; Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
R;Marekov, L.; Krook, M.; Joernvall, H.	Query Match 31.6%; Score 407.5; DB 1; Length 255; Best Local Similarity 39.0%; Pred. No. 3.8e-25; Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
FBS Lett. 266, 51-54, 1990	Query Match 31.6%; Score 407.5; DB 1; Length 255; Best Local Similarity 39.0%; Pred. No. 3.8e-25; Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
A;Reference number: S10707; MUID:90306362	Query Match 31.6%; Score 407.5; DB 1; Length 255; Best Local Similarity 39.0%; Pred. No. 3.8e-25; Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;
A;Status: preliminary	Query Match 31.0%; Score 400.5; DB 1; Length 255; Best Local Similarity 37.1%; Pred. No. 1.4e-24; Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;
A;Molecule type: protein	Query Match 31.0%; Score 400.5; DB 1; Length 255; Best Local Similarity 37.1%; Pred. No. 1.4e-24; Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;
A;Residues: 1-255 <MAD>	Qy 1 MSNRDLDRKVAVITGGTIGLATAKVEEGAKVMTDRHSVDGEKAKSVGTDPQIQFFQH 62 Db 1 MMNLITDKTVLTGGTGGAGIGTAVQARLQGQQNVVADIDEQAEVNRKEEN-DRHVF 59
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology	Qy 61 QHDSSDEDGWTKLFDATEKAFGPVSTLVNNAGIAVNKSVEETTAEWKRLLAVNLGDVFF 120 Db 60 QRDITDRAOHAVESAHVTFGDVLINNAGIEVTPAHIEMELSOKNQVQVNLTGMFL 119
C;Keywords: NAD; oxidoreductase	Qy 121 GTRLGJORMKNGNKGASLINNSIEGGVDPGLAYASKGAVRINSRSAAADCALRKYD 180
F;7-183/Domain: short-chain alcohol dehydrogenase homology <SADH>	

Db	120	MSKHALKHMILAGKG-NIINCSVGGLVAFDIPAYNASKGGVLQLTKNSWADYA--KHO	176	Qy	61	QHDSSDEDGWTKLFDATETKAEGPVSTLYNNAGIAVNKSVEETTAEWRLKLLAVNLDGFFF	120		
Qy	181	VRVNTYHPGYTKTPL---VDDLPQA-EAMSQRKIK-T-PGHIGEPPNDIAYICVYLASN	233	Db	58	RHDVSEADTFLVMAVORRGTFLAVLNVNNGAILLPGDMETGRLEFSRULKINTESVF1	117		
Db	177	IRVNCYCPGIDTPLENEKSGTLEETKKERAKVNPRLRGKPEETANVMEFLASD	236	Qy	121	GTRGLQRMKNGLGASLINMSSIEFGDLSGAYNAVGAVRIMSKAALDCALKDYD	180		
Qy	234	E SKFAGT GSEFWV DGGYTAQ	252	Db	118	GCQGQTAAMKE--TGSIIINNAVSVSWLPIEQAGYSASKA VASLTAAALSCRKQGYA	175		
Db	237	ISSYMTGSATADGGYTAQ	255	Qy	181	V-RVNTYHPGYTKTPLVD-DLP---GAEAMSQRKTPGMGHIGEPNDIAYICVYLASN	235		
RESULT 5									
3(or 17)beta-hydroxysteroid dehydrogenase (EC 1.1.1.51) - <i>Comamonas testosteronei</i> (ATCC 1				Db	176	IRRVSNTSHPDGIYTPTMRAOSDPKGYSKEMVLDPKLNTRAGYMPRIAQLVLFASDES	235		
C;Species: <i>Comamonas testosteronei</i>				Qy	236	KPATGSEFVVD	246		
A;Variety: ATCC 11996				Db	236	SVMGSELHAD	246		
C;Date: 14-Jul-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999				RESULT 6					
C;Accession: S48129; S51180; S15390; S6216; S62182				Qy	540755	hypothetical protein 5 - xanthobacter sp.			
R;Abalain, J.H.; di Stefano, S.; Quemener, E.; Abalain-Colloc, M.L.; Floch, H.				C;Species: Xanthobacter sp.					
J; Steroid Biochem. Mol. Biol. 44, 133-139, 1993				C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999					
A;Title: Cloning, DNA sequencing and expression of (3-17)beta hydroxysteroid dehydrogenase				C;Accession: S47055					
A;Reference number: S48129; MUID:9316721				R;Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.					
A;Accession: S48129				submitted to the EMBL Data Library, June 1994					
A;Molecule type: DNA				A;Description: Implementation of xanthobacter Py2 mutants in epoxyalkane degradation; e					
A;Residues: 1-254 <BAA>				A;Reference number: S47051					
A;Cross-references: EMBL:X633739,				A;Accession: S47055					
A;Note: the source is designated as <i>Pseudomonas testosteronei</i>				A;Molecule type: DNA					
R;Abalain, J.H.				A;Residues: 1-249 <SWA>					
submitted to the EMBL Data Library, November 1991				A;Cross-references: EMBL:X79863; NID:9520947; PID:CAA56245.1; PID:9520952					
A;Reference number: S511780				C;Superfamily: ribitol dehydrogenases; short-chain alcohol dehydrogenase homology					
A;Accession: S511780				F;5-181/Domain: short-chain alcohol dehydrogenase homology <SDAH>					
A;Molecule type: DNA				Query Match					
A;Residues: 1-13, VV, 16-254 <ABW>				Best Local Similarity					
A;Cross-references: EMBL:X633739; NID:9312918; PID:CAA44977.1; PID:g312919				Matches					
A;Note: the source is designated as <i>Pseudomonas testosteronei</i>				Score					
R;Yin, S.J.; Vegelopoulos, N.; Lundquist, G.; Joeravall, H.				391; Score 391; DB 2; Length 249;					
Eur. J. Biochem. 197, 359-365, 1991				38.9%; Pred. No. 7.6e-24;					
A;Title: <i>Pseudomonas</i> 3-beta-hydroxysteroid dehydrogenase. Primary structure and relation				Mismatches					
A;Reference number: S15390; MUID:91224127				105; Indels 10; Gaps 6;					
A;Accession: S15390				5 LDGKVAITITCTGTGIGLAIATKFKVEGAKYMTIDRHSVGEKAKS VGT PDPQIQFFQHQDS	64				
A;Molecule type: protein				2 LDAEVTATITGAGTGLAVHAAITAGVARYALIDRDGACQRAAAEFGA --AAWVGADV	59				
A;Residues: 2-40, 'E', 41-176, 178-240, 'G', 242-254 <XYN>				65 SDEDGWTKLFDATETKAEGPVSTLYNNAGIAVNKSVEETTAEWRLKLLAVNLDGFFF	124				
A;Note: the source is designated as <i>Pseudomonas testosteronei</i>				124: : : : : : : : : : : : : : : :					
R;Benach, J.; Knapp, S.; Oppermann, U.C.T.; Haegglund, O.; Joernvall, H.; Ladenstein, R.				60 TDEAAITAAMAGA QAGLGP LTGLVNGAGTAGFGSVTHATEVETWSRIMAVNYTGFLPLASKA	119				
Eur. J. Biochem. 236, 144-148, 1996				125 GIQRNKNKGAGSLINMSSIEFGDLSGAYNAVGAVRIMSKAALDCALKDYDVRVN	184				
A;Title: Crystalization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid				125: : : : : : : : : : : : : : : :					
A;Reference number: S62216; MUID:96184931				120 ALFGMUEERGGA-TVNGSYAGLGPHTMAYCARKGAVVNLTROMADYSGR--GIRVN	176				
A;Accession: S62216				185 TVHPGYIK-TPLVDDLPGAE--EAMSQR-TKTPMGHIGEPNDIAYICVYLASNESKFAT	239				
A;Status: nucleic acid sequence not shown; not compared with conceptual translation				239: : : : : : : : : : : : : : : :					
A;Accession: S62182				177 WVCPTGIVAGTDGMROLLGDPELEARLAKYPNRGTPE DIAEA VELLSTAAFTV	236				
A;Molecule type: DNA				237 GSVLAVDGGMATA 248					
A;Cross-references: EMBL:L08971; NID:9309859; PID:AAA25742.1; PID:g309866				RESULT 7					
A;Note: the source is designated as <i>Pseudomonas testosteronei</i>				E72427					
C;Keywords: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology				oxidoreductase, short chain dehydrogenase/reductase family					
F;2-254/Product: 3(or 17)beta-hydroxysteroid dehydrogenase #status experimental <MAT>				C;Species: <i>Thermotoga maritima</i>					
F;8-185/Domain: short-chain alcohol dehydrogenase homology <SDAH>				C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000					
Query Match	30.5%	Score 393; DB 2;	Length 254;	C;Accession: E72427					
Best Local Similarity	36.7%	Pred. No. 5.4e-24;		R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwynn, M.L.; Dodson, R.J.; Haft, D.H.; Hic					
Matches	92;	Conservative	49; Mismatches 100; Indels 10; Gaps 6;	Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.					
Qy	1	MSNRDGVIAITGTGIGLAIATKFKVEGAKYMTIDRHSVGEKAKS VGT PDPQIQFF	60	Nature 399, 323-329, 1999					
Db	1	MTNRLQGKVVALVTTGGAGSAGVGLVVKLIGSEGAKVAFSDINA-AGQOLAAELG--ERSMFV	57	A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome					
				A;Reference number: A72200; MUID:99287316					
				A;Accession: E72427					

A:Status:	Preliminary
A:Molecule type:	DNA
A:Residues:	1-256 <ARN>
A:Cross references:	GB:AE001690; GB:AE000512; NID:94980496; PIDN:AAD35113.1; PIDN:94980505
A:Experimental source:	strain MSB8
C:Genetics:	
C:Superfamily:	ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
Query Match	29.7%; Score 383; DB 2; Length 256;
Best Local Similarity	35.5%; Pred. No. 3.4e-23;
Matches	93; Conservative 48; Mismatches 95; Indels 26; Gaps 7;
RESULT 9	
Qy	5 LDGRVAVITGGTIGLIAITKEVEGAKVMTDRHSVG---EKAASKVGPDOIQPFQ 61
Db	2 LEGKVAVTGGCGCAGAAQALFAENGKVAIEDEAEGVEREEMLRLERGL--DVTFVK 59
Qy	62 HDSSDEDGTWTKLFDATEKAFGPVSITYLNRAVNAKSVETTAEWRKLLAYNLDGVEFG 121
Db	60 TDVADENSVKMVKRTKTVYGGDVNVNAAMSVKSFERPLEEWEVRVNLNTGPIC 119
Qy	122 TRGIORMKNGKLGASLINMSIEGFVGDPGLGAYNASKGAVRIMSKSAALDCALKDYD 181
Db	120 SRYCAEEMIKRG-GVITNIASTRAFOSEPTDEPEYPSASKGIVLAVALTHSLAV--SLSRYHI 176
Qy	182 RVNTVHPGYIKTKPLVDLPLGAEEGAMSQRTK-----PMGHIGEPNDIAYICVYLA 231
Db	177 RVVSISSPWET-----SENKKSSLRKPDLRPIDEHQHPAGRGNPLDIAHLCVFLA 229
Qy	232 SNE-SKPATGSEEFVWDGTYAQ 252
Db	230 DDEKAGFTITGTFNPIVDGGMTVK 251
RESULT 8	
E7040	probable fabG2 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species:	Mycobacterium tuberculosis
C:Date:	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession:	E70740
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holloway, S.; Rajaraman, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.	
A:Authors:	Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title:	Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number:	A70500; MUID:98205987
A:Accession:	E70740
A:Status:	Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type:	DNA
A:Residues:	1-247 <COL>
A:Cross references:	GB:275555; GB:AL123456; NID:93261608; PIDN:CAA99983.1; PIDN:g1419053
A:Experimental source:	strain H37RV
C:Genetics:	
A:Gene:	fabG2
C:Superfamily:	ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH> F:8-186/Domain: short-chain alcohol dehydrogenase homology <SDH>
Query Match	29.5%; Score 380; DB 2; Length 247;
Best Local Similarity	36.2%; Pred. No. 5.7e-24;
Matches	92; Conservative 52; Mismatches 94; Indels 16; Gaps 4;
RESULT 10	
Qy	1 MSNRDCKVATTTGGTIGLIAITKEVEGAKVMTDRHSVGKAASKVGPDOIQPFQ 60
Db	1 WASLNNARTAVITGGAGQLGAIQGRFVAEGARVVLGDVNLEATEAKRJGGDDVALV 60
Qy	61 QHDSSDEDGTWTKLFDATEKAFGPVSITYLNRAVNAKSVETTAEWRKLLAYNLDGVEFF 120
Db	61 RCDVTDADDVILITAVERRGGLDVMNNAGITRDATMRTEQFDQVAVHLKGTVN 120
Qy	121 GTRLGIGRMKNGKLGASLINMSIEGFVGDSLGAYNASKGAVRIMSKSAALDCALKDYD 180
Db	-121 GTRLAAAAMREKRRGA-TVNNSSSVSRGVYGMQTNYSAAKAGTIVGHTKAALKE--LAHLG 177

B95284

probable [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
C:Species: Sinorhizobium meliloti
C:Date: 24 Aug 2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: B95284
 R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Weiss, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti genome
 A;Reference number: 952622; PMID:21396509; PMID:11481432
 A;Accession: B9284
 A;Residues: 1-253 <RUR>
 A;Molecule type: DNA
 A;Superfamily: short-chain alcohol dehydrogenase homology
 A;Cross-references: GB:AE006469; PIDN:AAK64836.1; PID:914523249; GSPDB:GN00165
 R;Galibert, F.; Finan, T.M.; strain 1021, megaplasmid pSymA
 R;Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 292, 668-672, 2001
 A;Authors: Kahn, D.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Beaulieu, P.; Vandembroucq, M.; Vorholter, F.J.; Weidner, S.; Weiss, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Content: annotation
 C;Genetics
 A;Gene: Sm0329
 A;Genome: Plasmid
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.9%; Score 372.5; DB 2; Length 253;
 Best Local Similarity 37.7%; Pred. No. 2.3e-22;
 Matches 97; Conservative 46; Mismatches 93; Indels 21; Gaps 8;

Qy 1 MSNRDGVKAITGPGIGLIGIAITKFKVEGAKVATIDRH---SDVGEGAKSVGTPDQ 56
 Db 1 MKREPGKVAIVTGGGSGIGMAANRLLEGASTYMSGRTEKRLSDVASKM---PADR 55
 Qy 57 IQFFHDSSDEDGNTKLFDTEAKAFGPVSTLVNNAGIAYNSVEETTTAERKLLAVNL 116
 Db 56 SGIFTYANVSSPRDCALVALAATVERGRIDTVNAAGMNFTGQTQTSDDPDECASDL 115
 Qy 117 GVFFGTRLGIORMK_NKGIGASINIMSSIEFGDPGIGAYNASKGAVRIMSKSALDCA 175
 Db 116 GVFYMSRAAYPHLKETKG---SIVNGISVSSLGGMWSHANYAARGVANLRTSAA--CD 170
 Qy 176 LKDYDVRVNTVHPGTYKTPLYDLEGAEEAMSQRQT--KTPMGHIGEPNDIAYICVYLAS 233
 Db 171 LGKEFVRYANTVAPGLTVPTVGHYEAMD-DDALEXAKWDRFLRRAGQP---ASAVFLASD 226
 Qy 234 ESKPATGSEFVVDGGYT 250
 Db 227 EAATGIVLPVDGGGT 243

RESULT 12
 A33528
 C;Species: Bacillus megaterium (EC 1.1.1.47) - Bacillus megaterium
 C;Date: 29-Jun-1990 #sequence_revision 29-Jan-1990 #text_change 11-Jun-1999
 C;Accession: A33528
 R;Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
 J. Biol. Chem. 264, 6381-6385, 1989
 A;Title: Stability-increasing mutants of glucose dehydrogenase from *Bacillus megaterium*
 A;Reference number: A33528; MUID:89197943
 A;Accession: A33528
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-261 <RUR>
 A;Cross-references: GB:J04805; NID:9142974; PID:AAA22475.1; PID:9142975
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: oxidoreductase
 F;8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.7%; Score 370.5; DB 2; Length 261;
 Best Local Similarity 33.6%; Pred. No. 3.5e-22;
 Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;

Qy 1 MSNRDGVKAITGPGIGLIGIAITKFKVEGAKVMT----DRHSVDGEKAAKSVGTPD 55
 Db 1 MYKDLEGKVVVTGGSMAIRFATEKAVVYVNRSKEDEANSVLEBIIKKYGEAI 60
 Qy 56 QIOFFHDSSDEDGNTKLFDTEAKAFGPVSTLVNNAGIAYNSVEETTTAERKLLAVNL 115
 Db 61 AV---KGDTVYESDVINLYQSAIKEPGKLDOMINNAGLENPVSSHEMSLSDWNKYIDTNL 117
 Qy 116 DGFFGTRLGIORMK_NKGIGASINIMSSIEFGDPGIGAYNASKGAVRIMSKSALDCA 175
 Db 118 TGAFLGOSREAKYKFENDITGTVINSSVHERKIPPLFVHAAKSGKMLTETLLEYA 177
 A;Reference number: 139850
 A;Accession: 139852
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-261 <RBS>
 A;Cross-references: GB:p00043; PIDN:BA14099.1; PID:9216268
 A;Description: catalyzes NAD(P)-dependent dehydrogenation of D-glucose.
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: oxidoreductase
 F;8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>

RESULT 13
 B86737
 acetoin dehydrogenase (EC 1.1.1.5) [imported] - *Lactococcus lactis* subsp. *lactis* (str

N:Alternate names: acetoin reductase
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 *sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: B86737
 R:Boletin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarrie, R.; Weissenbach, J.; Ehrlich, S.; Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss 11
 A:Reference number: A86625; PMID:21235186; PMID:11337471
 A:Status: preliminary
 A:Molecule type: DNA
 A:Cross-references: GB:AE005176; PID:912723829; PIDN:AAK04996.1; GSDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C:Keywords: butyrate; oxidoreductase

Query Match 28.5%; Score 368; DB 2; Length 253;
 Best Local Similarity 34.3%; Pred. No. 5.3e-22;
 Matches 86; Conservative 48; Mismatches 103; Indels 14; Gaps 4;
 Result 15

Db 3 KIAVATGQGQIGPFAIKRLYNGPKVALIDINBETAKAAKEDG--ENSFAKTDYSDR 60
 Qy 68 DGGTAKLFDATKEAFGPVSTLVNNNAGIAYNKSVEETTAEWRKLLAVNLDFGPFGTRGQ 127
 Db 61 EDVISA NAVDRFQDLN VNNNAGIAPTTQIETITPQFHQVNYNNVGGVLMGTOSTA 120
 Qy 128 RMNKLEGASIIIMSSISFGVDFPSLGAYNASIGAVRIMSksALDALKIDFVRNTVH 187
 Db 121 LEFKLHGCGKKNATNSQVGNPMLMYSKSKFAVGMKAARD--LAEGITVNAYA 178
 Qy 188 PGWIKTPLYVDL-----PGAEAMSORT --KTPMGHIGEPNDIAYICVYLASFKE 237
 Db 179 PGWIKTPHDFIAHQVKGNAGRDDEWGMOFAKDIAMKRLESEPDVANVVSFLAGPDSNY 238
 Qy 238 ATGSEFVYDG 248
 Db 239 IRTQTIIVDG 249

Query Match 26.1%; Score 366; DB 2; Length 272;
 Best Local Similarity 35.4%; Pred. No. 8.4e-22;
 Matches 91; Conservative 44; Mismatches 108; Indels 14; Gaps 6;

Db 3 RLENKVAVTVGASTGIGASAIALAQEAYVLAVIDAERAVSETVDKIRSNGDNIAKRNVD 62
 Qy 4 RLDGKVALITGGTGLIGILIAIATRFVEGAKYMTDRHSVGERKAAKSVGTPDQJQFRQHD 63
 Db 64 SSDEDGWTKLFDATKEAFGPVSTLVNNNAGI--AVNKSVETTAEWRKLLAVNLDFYFFG 121
 Db 63 ISBQQVQDFVSDIKEOFRIDYLFLNAGDVNAAGR-IHEYPIDVYKIMNTDMRGTLIM 121
 Qy 122 TRIGIQMKNNKGASIIIMSSISFGVDFPSLGAYNASIGAVRIMSksALDALKIDYDV 181
 Db 122 TCKMLPLMMNO--GGSVNTNTSSFSGQAEIDLRSGYNNAKGVINFTSIAIEVG-RD-GI 177
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; PMID:98295987
 A:Accession: C70885
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-258 <CDS>
 A:Cross-references: GB:AL008883; GB:AL123456; NID:93261490; PIDN:CAA1519.1; PID:9261280
 C:Genetics:
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology <SDH>
 F:1-188/Domain: short-chain alcohol dehydrogenase homology <SDH>

Query Match 28.4%; Score 367; DB 2; Length 258;
 Best Local Similarity 35.7%; Pred. No. 6.5e-22;
 Matches 92; Conservative 45; Mismatches 105; Indels 16; Gaps 7;

Db 235 SKFATGSEFVYDGTYA 251
 Db 238 SSEPITGETIRDGVM 254

Search completed: October 30, 2002, 15:46:26
 Job time : 22 secs

GenCore version 5.1.3
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CM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 12 Seconds
 (without alignments)
 813.111 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 1290

Sequence: 1 MNRLDGKVALITGGTIGIG.....NESKFATGSEFVYDGGYTAQ 252

Scoring table: BLOSUM462
 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	464.5	36.0	260	1	YK02_MYCTU	Q10855 mycobacteri
2	441.5	34.2	250	1	LJNY_PSEPA	P50198 pseudomonas
3	407.5	31.6	255	1	2BHD_STREX	P19992 streptomyce
4	400.5	31.0	255	1	YWFD_BACSU	P39640 bacillus su
5	383	29.7	256	1	Y019 THEMMA	Q56318 thermotoga
6	380	29.5	247	1	YD50_MYCTU	Q11020 mycobacteri
7	371.5	28.8	261	1	DHGL_BACME	P39482 bacillus me
8	370.5	28.7	261	1	DHG_BACME	P40288 bacillus me
9	370	28.7	253	1	3BHD_CORTIE	P19871 comamonas t
10	365.5	28.3	246	1	FABG_THEME	P9x248 thermotoga
11	363.5	28.2	261	1	DHGA_BACME	P10528 bacillus me
12	360	27.9	262	1	DHGB_BACME	P07999 bacillus me
13	358.5	27.8	261	1	DHG_BACSU	P12310 bacillus su
14	357.5	27.7	261	1	DHGA_BACME	P39485 bacillus me
15	355.5	27.6	261	1	DHG2_BACME	P39483 bacillus me
16	352.5	27.3	261	1	DHG3_THEME	P39484 bacillus me
17	351.5	27.2	251	1	Y325_THEME	Q9wygo thermotoga
18	348.5	27.0	258	1	DHG_BACSU	P80869 bacillus su
19	345	26.7	261	1	DHB8_HUMAN	P92506 homo sapien
20	339.5	26.3	256	1	BUDC_KLEPN	Q48436 klebsiella
21	326	25.3	285	1	G539_BACSU	P80873 bacillus su
22	325.5	25.2	260	1	DHBB_MOUSE	P50171 mus musculu
23	324	25.1	336	1	TS2_MAIZE	P50160 zea mays (m-
24	322	25.0	289	1	YHDF_BACSU	007575 bacillus su
25	321	24.9	248	1	FABG_CHLNP	Q9pkf7 chlamydia m
26	321	24.9	548	1	YAVI_RHEUS	Q53217 rhizobium s
27	319.5	24.8	256	1	GNO_GLIOX	P50199 gluconobact
28	319.5	24.8	258	1	BDHA_RHIME	P86034 rhizobium m
29	318	24.7	244	1	FABG_VIBCH	Q9kqhf7 vibrio chol
30	317.5	24.6	262	1	VER1_ASPPA	P50161 aspergillus
31	317	24.6	241	1	PHBB_ZOOXA	P23238 zoogloea ra
32	316	24.5	245	1	FABG_BACSU	P51831 bacillus su
33	316	24.5	281	1	S001_CANAL	P87219 candida alb

ALIGNMENTS

RESULT	1	YK02_MYCTU	STANDARD;	PRT;	260 AA.
ID	YK02_MYCTU				
AC	Q10855;				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DB	putative oxidoreductase Rv2002	(EC 1.1.1.1).			
GN	FABG3 OR RV2002 OR MT2058 OR MTCY39	16C.			
OS	Mycobacterium tuberculosis				
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OC	NCBI_TAXID=1773;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=H37Rv;				
RX	MDLINER=98395987; PubMed=9634230;				
RA	Gordon S.V., Broesch R., Parrill J., Garnier T., Churcher C., Harris D., Cole S.T., Badcock K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devilin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Sulston J.E., Whitehead S., Barrell B.G.; Deboy R., Dodson R., Feltwell T., Gentles S., Hamlin N., Holroyd S., Murphy L., Sulston J.E., Whitehead S., Barrell B.G.; Delcher A., Utterback T., Weidman J., Khoury H., Gill J., Mikula A., Bishai W.; White genome comparison of Mycobacterium tuberculosis from the complete genome sequence. ; RT				
RA	*Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. ; RT				
RA	complete genome sequence. ; RT				
RA	Nature 393:537-544(1998). ; RT				
RA	SEQUENCE FROM N.A. ; RP				
RA	STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Allard D., Elsen J.A., Carpenter L., White O., RA				
RA	Peterson J., DeBoy R., Haft D., Hickey E., Kolonay F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Deicher A., Utterback T., Weidman J., Khoury H., Gill J., Mikula A., Bishai W.; RT				
RA	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains." ; RT				
RL	Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases. ; RL				
CC	1-SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY. ; CC				
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CC	--				
DR	CNA98114.1; AE007057; AAK46351; -; DR				
DR	EMLBL; AE007057; AAK46351; -; DR				
DR	HSSP; P19592; 1HDC. ; DR				
DR	TIGR; MT2058; -; DR				
DR	Tuberclist; RV2002; -; DR				
DR	Interpro; IPR002198; ADH_short. ; DR				

DR	Pfam: PF00106; adh_short; 1.	DR	HSSP: P19992; IHDC.
DR	PRINTS; PR00080; SDRFAMILY.	DR	InterPro: IPR002198; ADH_short.
DR	PROSITE; PS00061; ADH_SHORT; 1.	DR	Pfam: PF00106; adh_short; 1.
KW	Hypothetical protein; Oxidoreductase; NAD; Complete proteome.	DR	PRINTS; PR00080; SDRFAMILY.
FT	11 35 NAD (BY SIMILARITY).	DR	PROSITE; PS00061; ADH_SHORT; 1.
FT	153 153 NAD (BY SIMILARITY).	KW	Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT	174 174 S -> G (IN REF. 2).	FT	NAD (BY SIMILARITY).
SEQUENCE	260 AA; 27030 MW; 0935A14ED3620B7 CRC64;	FT	BY SIMILARITY.
Query Match	36.0%; SCORE 464.5; DB 1; Length 260;	SQ	250 AA; 25492 MW; 8C52703FF76382CF CRC64;
Best Local Similarity	42.2%; Pred. No. 6.6e-31; Mismatches 90; Indels 11; Gaps 5;	Query Match	34.2%; Score 441.5; DB 1; Length 250;
Matches	106; Conservative 44; Mismatches 93; Indels 15; Gaps 6;	Best Local Similarity	41.0%; Pred. No. 4.7e-29;
Qy	1 MSNRLDGKVIAITGGTIGLALATKVEGAKVMTDRHSVGEAKSVGTPDQIOFF 60	Matches	105; Conservative 43; Mismatches 93; Indels 15; Gaps 6;
Db	1 MSGRLIGKVVALVSGARGNGASHIVRANYAEGAVKVFGLDEEGKAVAYELA-DARRYV 58	Qy	1 MSNRLDGKVIAITGGTIGLALATKVEGAKVMTDRHSVGEAKSV----STPD 55
Qy	61 QHDSSDEDGWTKLDFDATAKAFGPVSTLYNNAGIAVNKSVEETTAENRKLLAVLNLDGVFF 120	Db	1 MAURLAGKVVALTGGASIGUAQAKRAFEAEKGAKVVI-GDLNEEAKGVVAEIRAGG 56
Db	59 HLDVTPQAWTAATDVTAFFGLHLVLNNAAGILNLIGTIEDALTEQRILDVNLTGVFL 118	Qy	56 QIOFFQHQSSDEDGWTKLDFDATAKAFGPVSTLYNNAGIAVNKSVEETTAENRKLLAVLNLDGVFF 115
Qy	121 GTRGIORMKNGKGASTINMSSIEGFYGDPSLGAYNASKAVRIMSKSAALDCALKDYD 180	Db	57 DAFLFIRDVDTDAASWNNAIAAVDGFGLLTLSNTAGIHPGGFEESIEGPNKMYAVNO 116
Db	119 GIRAVVKPMKEAGRGS-TINNISLEGLATGTVACHGTATKAFAVRGTKSTALE-LGPSC 175	Qy	116 DGYFFGTRIGIORMKNGKGASTINMSSIEGFYGDPSLGAYNASKAVRIMSKSAALDCA 175
Qy	181 VRVNTVHFGYIKTPVLDLPGABEAMSORTKPPMGHIGEPNDIAYICVYLASNEKFATG 240	Db	117 TAFLGLTKAAIPLVKSGNG-SIINISLIGHPTGNASYCATKAVRIMSKAAALE-- 173
Db	176 IRVNSIHFPGLVKTPMTOVY-EDIF---QPALGRAAEPVEVSNLVVYLASDESSYISTG 229	Qy	176 LKDYDVRYNTVHFGYIKTPVLDLPGABEAMSORT-KTPMGHIGEPNDIAYICVYLASNE 234
Qy	241 SEFVVDGTYA 251	Db	174 FVDRGVRYNTVHFGMNTPITANVY-PDVLKQQTSSQIPGMKLQDPDIANGALFLASDE 231
Db	230 AEEVVDGTVVA 240	Qy	235 SKFATGSEFVVDGTY 250
Db	232 AKYITGVLDLPIDGWS 247	Db	232 AKYITGVLDLPIDGWS 247
RESULT 2			
LINK_PSEPA	STANDARD; PRT; 250 AA.	RESULT 3	
ID	LINK_PSEPA	ID	2BHD_STREX
AC	P50198;	AC	P19992.
DT	01-OCT-1996 (Rel. 34, Created)	DT	01-FEB-1991 (Rel. 17, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)	DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)	DT	01-NOV-1997 (Rel. 35, Last annotation update)
DB	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.1.53).	DE	20 beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
DB	(2,5-dDOL dehydrogenase).	OS	Streptomyces exfoliatus (Streptomyces hydrogenans).
GN	LINK.	OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OS	Pseudomonas paucimobilis (Sphingomonas paucimobilis).	OC	Actinomycetales; Streptomyceae; Streptomyces; Streptomyces.
OC	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;	OX	NCBI_TaxID=1905;
OX	Sphingomonas.	RN	[1]
RN	NCBI_TaxID=13689;	RP	SEQUENCE.
RP	SEQUENCE FROM N_A.	RX	Medline: 90306362; PubMed: 2194840;
RC	STRAIN_INUT26;	RA	Marekov L., Krook M., Joenvall H.;
RX	Medline: 94-22977; PubMed: 7515041;	RT	"Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RA	Nagata Y., Ohtomo R., Miyazaki K., Fukuda M., Yano K., Takagi M.;	RA	"short-chain, non-metallooenzyme alcohol dehydrogenase type.";
RT	Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase gene involved in degradation of gamma-hexachlorocyclohexane in <i>Pseudomonas paucimobilis</i> . ;	RA	"Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid dehydrogenase: a member of a short-chain dehydrogenase family.";
RT	J. Bacteriol. 176:3117-3115 (1994).	RL	Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068 (1991).
CC	-1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL INTO 2,5-DICHLOROHYDROQUINONE (2,5-DHQ). LINK IS NOT ESSENTIAL TO GAMMA-HCH DEGRADATION.	CC	-1- CATALYTIC ACTIVITY: Androstan-3-alpha,17-beta-diol + NAD(+) = 17-
CC	-1- PATHWAY: DEGRADATION OF GAMMA-HXACHLOROCYCLOHEXANE.	CC	-1- SUBUNIT: HOMOTETRAMER.
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC	CC	DR	PDB: 2HSD; 31-AUG-94.
CC	CC	DR	PDB: 1HDC; 07-FEB-95.
CC	CC	DR	InterPro: IPR002198; ADH_short.
CC	CC	DR	Pfam: PF00106; adh_short; 1.
DR	EMBL: D23722; BAA04939.1. -	DR	Prints: PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.
 RW Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
 FT NP_BIND 10 34 NAD (BY SIMILARITY).
 FT ACT_SITE 152 152 NAD OR NADP (BY SIMILARITY).
 SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;

Query Match 31.6%; Score 407.5; DB 1; Length 255;
 Best Local Similarity 39.0%; Pred. No. 2.8e-26;
 Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;

Qy 3 NRDGKVATITGGTUGIGLATAKTFVEGAKVMSYGTDPQIOFFOH 62
 Db 2 NDLSGKTVITGGTARGLGAAERQAVAGRNVLADVLDEGAATARELG--DAARYQHL 59
 Qy 63 DSSDEGWTKLFDTEKAEGFPTVSTLYNNACIAVNKSVEETTAEWRKLLAVNLGVFFGT 122
 Db 60 DVTIEEDWQRVAYAREEFGSDGLVNNAAGTSTGMFLFETESVERFRKVYDINLNQFEGIM 119
 Qy 123 RFLGIORMKNGKLGASTINMSSIEGFVGPDPGLAYNASKGAVRIMSKSAALDCALKDYDVR 182
 Db 120 KTVIPAMKDAG-GGSTVNTISSAAGLMGLAATTSIGASKNCVRLSKLAVNE--LGTDRIR 176
 Qy 183 VNTVHPGYIKPLVDDOLPGAEAMASQRTKTPMGHIG-EPNDIATCYVLASNESKFATGS 241
 Db 177 WNSVHEGMITYPPMATE-TGIRQEGNYNPNTPMGRVNEPGEIAGAVKVLISDTSSYTGA 235
 Qy 242 EFWVDDGGYT 250
 Db 236 ELAVDGGWT 244

RESULT 4
 YWFD_BACSU
 ID YWFD_DACSU STANDARD PRT; 255 AA.
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE Hypothetical oxidoreductase ywfd (EC 1.1.1.1).
 GN YWFD OR IPA-2D.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-95020517; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
 RA Presecan E., Santana M., Sibachinski E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus" genome project: cloning and sequencing of the 97
 kb region from 325 degrees to 333 degrees.";
 RL Mol. Microbiol. 10:371-384 (1993).
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.

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CC DR EMBL; X73124; CAA51638.1;
 CC DR EMBL; Z99123; CAB15799.1;
 CC DR PIR; S39737; S39737;
 CC DR HSSP; P50162; IA1;
 CC DR Subtilist; BG10628; YwfD;
 CC DR InterPro; IPR002198; ADH_short;
 CC DR Pfam; PF00106; adh_short; 1;

DR PRINTS; PRO0080; SDRFAMILY.
 DR PROSTE; PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Complete proteome.
 FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 SQ SEQUENCE 255 AA; 27324 MW; 20A2259BFB88C9B CRC64;
 Query Match 31.0%; Score 400.5; DB 1; Length 255;
 Best Local Similarity 37.1%; Pred. No. 1e-25;
 Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;
 Qy 1 MSNRDLGKVALITGGTIGIGLATAKTFVEGAKVMSYGTDPQIOFFOH 60
 Db 1 MIMNLTDKTVLITGGASIGCYAAQAFQLQANVYVADIDEAQGAMMRKENN-DRLHFV 59
 Qy 61 QHDSSDBDGTTKLFDTAEKAFGPVSTLVNNGIAVNKSVEETTAEWRKLLAVNLGVFF 120
 Db 60 QTDIDDEAQCNAVESAVAHPPGGLDVLLNNAGIEVAPIHEMELSDWNKYLQVNNTGMFL 119
 Qy 121 GTRUJLQRMKNKGLGASIIINMSSIEGFVGPDPGLAYNASKGAVRIMSKSAALDCALKDYD 180
 Db 120 MSKHALKHMIAAGKG-NIINTCSYVGGLVLPDIPAYNASKGGVLOLKTSKHAVIDYA--KHQ 176
 Qy 181 VRVNTVHPGYIKPLVDDOLPGAEAMASQRTKTPMGHIG-TPMGHICEDPDNIAVICYLASN 233
 Db 177 IRVNVCYCPGLDTPLNEKSLEENNSTEETKKERAKVNPLRLGKPEETANVMLFLASD 236.
 Qy 234 ESKPATGSEFVVDGGYTAQ 252
 Db 237 LSSTMTGSAITADGGTAQ 255

RESULT 5
 Y019_THEME
 ID Y019_THEME STANDARD PRT; 256 AA.
 AC Q56318;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase TM0019 (EC 1.1.1.1).
 GN TM0019
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSBB / DSM 3109;
 RX MEDLINE=95020516; PubMed=8550425;
 RX Kletzin A., Adams M.;
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald K.E., Clayton R.A., Gill S.R., Dodson R.J., Gwynn M.L.,
 RA Raft D.H., Utterback T.R., Malick J.A., Lillier K.D., Garrett W.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSBB / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J.,
 RA Kletzin A., Adams M.;
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald K.E., Clayton R.A., Gill S.R., Dodson R.J., Gwynn M.L.,
 RA Raft D.H., Utterback T.R., Malick J.A., Lillier K.D., Garrett W.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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 CC or send an email to licensed@isb-sib.ch).

CC EMBL: X85171; CAA59459; 1.
 DR AE001690; AAD15113; 1.
 DR HSSP: P19992; 1HDC.
 DR TIGR: TM0019; -.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR HYPOTHETICAL PROTEIN: Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 BY SIMILARITY.
 FT ACT_SITE 153 153 RGGGIVL->TRVRSDH (IN REF. 1).
 FT CONFLECT 130 136 MW: D68160BALD7980C6B CRC64;
 SQ SEQUENCE 256 AA; 28078 MW; 29.7% Score 383; DB 1; Length 256;
 Best Local Similarity 35.5%; Pred. No. 2.8e 24;
 Matches 93; Conservative 48; Mismatches 95; Indels 26; Gaps 7;

Qy 5 LDGRVAVITGGTIGIGLATAKVEEGAKVMTDRHSVG--EKAAKSGVTPPDQIQPFQ 61
 Db 2 LEGRAVVTGGCGOGIAATAQLEPAENGKVKVIAEIDEPAGVEREEMLERGLI--DVPEPVK 59

Qy 62 HDSSDEGTWTKLDATEKAFGPYSTLVNNIAVNSKVEETTAEWKLAVNLGDGVFF 121
 Db 60 TDVADENSYKNMTRKTVEIYGGDVLYRNAAVMSVKSFERPLEEVIRVNLTGPIC 119

Qy 122 TRGIQRKRNKGJGASITINMSSIEFGVGDPSLGAYNASKGAYRIMSKSAALJCALKYDV 181
 Db 120 SRYCAEEMIKRG-GGVIINIASTRAFOSEPTDPYPSASKGLVALHTSLAV -SLSRYHI 176

Qy 182 RVNTVHPGIXTKPLVDDLPGEAEAMSORTKT-----PMGHIGEPNDIAYCYLLA 231
 Db 177 RVSISPEWIE-----SENKKKSLEKKPLRPIDHEQHPAGRVCNPLDIAHLYFLA 229

Qy 232 SNE-SKEPATGSEEVVDGCGYTAQ 252
 Db 230 DDEKAGFTTGTTNPVIDGGMVTK 251

RESULT 6
 YD50_MICTU ID YD50_MICTU STANDARD; PRT; 247 AA.
 AC Q11020; DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase; Rv1350 (EC 1.1.1.1).
 GN FABG OR RV1350 OR MT1393 OR MTG02B0.14.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Actinomycetidae;
 OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98395987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglemeier K., Gas S., Barry C.E., III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence," Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RESULT 7
 DHG1_BACME ID DHG1_BACME STANDARD; PRT; 261 AA.
 AC P39482; DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1 dehydrogenase I (EC 1.1.1.47) (GLCDH-I).
 GN GDIH.
 OS Bacillus megaterium.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Sporeforming group; Bacillus.
 OX NCBI_TAXID=1404;
 RN [1]

RESULT 9		Best Local Similarity 35.6%; Pred. No. 3.2e-23; Matches 89; Conservative 49; Mismatches 102; Indels 10; Gaps 6;	
3BHD_CONTE			
ID	3BHD_CONTE	STANDARD;	PRT;
AC	P19871;	253 AA.	
DT	01-FEB-1991 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	beta-hydroxysteroid dehydrogenase (EC 1.11.1.51).		
DE	Comamonas testosteronei (Pseudomonas testosteronei).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Comamonadaceae; Comamonas.		
OX	NCBI_TAXID=285;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	STRAIN=ATCC 11996;		
RX	MEDLINE=93176721; PubMed=8382516;		
RA	Abalain J.H., di Stefano S., Amet Y., Quemener E.,		
RA	Abalain-Colloc M.L., Floch H.H.,		
RT	"Cloning, DNA sequencing and expression of (3-17)beta hydroxysteroid dehydrogenase from Pseudomonas testosteronei."		
RT	J. Steroid Biochem. Mol. Biol. 44:133-139(1993).		
RL	[2]		
RN	RN		
RP	SEQUENCE.		
RX	MEDLINE=91224127; PubMed=2026158;		
RA	Yin S.-J., Vagelopoulos N., Lundquist G., Joernvall H.,		
RT	Pseudomonas 3 beta-hydroxysteroid dehydrogenase. Primary structure and relationships to other steroid dehydrogenases.";		
RT	Eur. J. Biochem. 197:359-365(1991).		
RN	[3]		
RC	CRYSTALLIZATION		
RX	STRAIN=ATCC 11996;		
RX	MEDLINE=96184894; PubMed=8617258;		
RA	Benach J., Knapp S., Oppermann U.C.T., Haegllund O., Joernvall H., Ladenstein R.,		
RA	"Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid dehydrogenase from Comamonas testosteronei ATCC 11996."		
RT	Eur. J. Biochem. 236:144-148(1996).		
RT	-1- CATALYTIC ACTIVITY: testosterone + NAD(P)(+)= androst-4-ene-3,17-dione + NAD(P)H.		
CC	-1- SUBUNIT: HOROTERAMER.		
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.		
CC	-1- DATABASE: NAME=Worthington enzyme manual;		
CC	WWW="http://www.worthington-biochem.com/manual/R/STDH.html".		
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CC	DR	EMBL; X653379; CAA44977.1; -.	
DR	PIR; S15390; S15390.		
DR	HSSP; P18992; 1HDC.		
DR	InterPro; IPR002198; ADH_short.		
DR	Pfam; PF00106; adh_short; 1.		
DR	PRINTS; PRO0000; SDRFAMILY.		
KW	Oxidoreductase; NAD; Steroid metabolism.		
FT	INT_MET 0 0		
FT	NP_BIND 10 34	NAD (BY SIMILARITY).	
FT	ACT_SITE 150 150	BY SIMILARITY.	
FT	CONFLICT 13 14	VV > GG (IN REF. 2).	
FT	CONFLICT 39 39	N > NE (IN REF. 2).	
FT	CONFLICT 177 177	MISSING (IN REF. 2).	
FT	CONFLICT 240 240	S > G (IN REF. 2).	
FT	SEQUENCE 253 AA; 26932 MN; CB677D921458B39 CRC64;		
CC	1		
CC	2		
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T	ACT_SITE	154	154	BY SIMILARITY.
Q	SEQUENCE	26401 AA;	26401 MW;	8C08904D28099142 CRC64;
	Query Match	28.3%	Score 365.5;	DB 1; Length 246;
	Best Local Similarity	35.1%	Pred. No. 7.1e-23;	
	Matches	87;	Conservative	52; Mismatches 100; Indels 9; Gaps
Y	4	RLDGKVAITITGGTLGIGLAIATKPYEEGAKYMITDRHSVDGERAAKSV-GTPDQIQFFQH	62	
b	2	RLEGRVKLTCIATGAASGIGKATLLFAEQEGATVAGDISKENLDSLVKEAGLPGKVDEYVL	61	
Y	63	DSSDEDGWFLPFLFDATEKGPVSTLYNNAGTAVNKSEVEETTAEWKLALAVNLGDYV	122	
b	62	NVTDRDQIKEVKEVYYQKGRIDLYNNAGITRDALLVRMKBEDWDAVINVNLKGVNNT	121	
Y	123	RLGIORMKNGLGASTINMSSIEGFYGDPDSLGLAYNASKGAVRIMSKSAALDCALKDYVR	182	
b	122	QMVPYPMIKORG-SIVNVSSVVGPNCGTNYAASKAGVIGMTKTKWAKELAGR--NIR	178	
	183	VNTVHPGYIKTPLVDDLP--GAEAMSQRITKTPMGHIGEPNDIAVTCVYLNASNEKFATG	240	
b	179	VNAVAPGFEIPTMTEKLPKARETALS--RIPLGRFGKPEEAVQVILFLASDESSVTG	235	
Y	241	SEFYVDDG 248		
b	236	QVIGIDG 243		

SEQUENCE FROM N.A.
STRAIN=M1286;
MEDLINE=80271315; PubMed=3134196;
Heilmann H.J., Maegert H.J., Gassen H.G.;
"Identification and isolation of glucose dehydrogenase genes of
Bacillus megaterium M1286 and their expression in Escherichia coli.";
Eur. J. Biochem. 174:85-90(1988).
-1 CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)= D-glucono-1,5-
lactone + NAD(P)H.
-1 SUBUNIT: HOMO-TRIMER.
-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.

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EMLBL; AL432; CAA30351.1; -.
PIR; S00012; S00012.
HSSP; P50162; IAEI.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PRO0080; SDIFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase; NADP+_Multigene family.
NP_BLAST_SITE    11      35      NADP (BY SIMILARITY).
ACT_SITE         158     158      BY SIMILARITY.

```

RESULT 12				
	DHGB_BACME	STANDARD;	PRT;	262 AA.
ID	DHGB_BACME			
AC	P07939;	Rel. 08, Created		
DT	01-OCT-1988	(Rel. 34, Last sequence update)		
DT	01-OCT-1989	(Rel. 12, Last annotation update)		
DT	01-OCT-1996	(Rel. 34, Last annotation update)		
DE	Glucose 1-dehydrogenase B	(EC 1.1.1.47).		
GN	GDBB			
OS	Bacillus megaterium			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Bacillus;			
OX	NCBI_Taxid=1401;			

RP SEQUENCE.
 RX MEDLINE=84108870; PubMed=6420184;
 Jany K.-D., Ulmer W., Froeschle M., Pfleiderer G.;
 "Complete amino acid sequence of glucose dehydrogenase from *Bacillus megaterium*."
 FEBS Lett. 165:6-10(1984).
 [2]
 RL RN REVISIONS TO 207 AND 258.
 RP MEDLINE=88271315; PubMed=3134196;
 Jany K.-D.
 RA Unpublished results, cited by:
 RL Heilmann H.J., Maegert H.J., Gassen H.G.;
 Eur. J. Biochem. 174:485-490(1988).
 RL RN SEQUENCE OF 1-52 FROM N.A.
 RP STRAIN=M1286;
 RC MEDLINE=88271315; PubMed=3134196;
 RA Heilmann H.J., Maegert H.J., Gassen H.G.;
 "Identification and isolation of glucose dehydrogenase genes of *Bacillus megaterium* M1286 and their expression in *Escherichia coli*."
 RL Eur. J. Biochem. 174:485-490(1988).
 [4]
 RN SEQUENCE OF 27-204.
 RP MEDLINE=84004396; PubMed=6413208;
 RX Ulmer W., Froeschle M., Jany K.-D.;
 RA "Evidence for an essential histidine residue in glucose dehydrogenase from *Bacillus megaterium* and sequence analysis of the peptides labeled with bromoacetyl pyridine."
 RT Eur. J. Biochem. 136:183-194(1983).
 RN

RX MEDLINE=84285362; PubMed=6432532;

RA Froschle M., Ulmer W., Jany K.-D.; "Tyrosine modification of glucose dehydrogenase from *Bacillus* tetrameric. Effect of tetranitromethane on the enzyme in the tetrmeric and monomeric state." Eur. J. Biochem. 142:533-540(1984).

RL -I- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)= D-glucono-1,5-lactone + NAD(P)H.

CC -I- SUBUNIT: HOMOTRIMER.

CC -I- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.

CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC PIR; S02289; S02299.

DR PIR; S01227; S01227.

DR PIR; A20238; A20238.

DR PIR; B20238; B20238.

DR PIR; C20238; C20238.

DR PIR; D20238; D20238.

DR PIR; A23260; A23260.

DR HSSP; P50163; 2AE1.

DR InterPro; IPR002190; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PRO0080; SDR_FAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NADP; Multigene family; sporulation.

FT NP_BIND 11 35 NADP (BY SIMILARITY).

FT ACT_SITE 160 160 BY SIMILARITY.

SO SEQUENCE 262 AA; 28347 MW; C9281328D634E789 CRC64;

Query Match Score 360; DB 1; Length 262; Best Local Similarity 34.8%; Pred. No. 2.2e-22; Matches 88; Conservative 51; Mismatches 106; Indels 12; Gaps 6;

Qy 1 MSNLDLGKVAITTGTGIGLATAKTFVEEGAKVMIT----DRHSVDGEKAKSVCPTPD 55

Db 1 MYKDLGEGYTVVITGTSSTGLGKSAIRFATEKAVVVNTRSKEDBANSVLEEKKVG-G 58

Qy 56 QIOFFQHDSSEDEGWTKLFDATKEAFGPYSTLVNNAGIAVANKSWEETTAEWKKLLAYNL 115

Db 59 EAIAVKGDVTVESDVINLVQSAIKEFGKLIDVMINAGHENPVSHMELSDWKVIDNL 118

Qy 116 DGFFGTRIGIQRMKNGKGASLNNMSST-EGFVGDPISLGAYNASKGAVRIMSKSAAALDC 174

Db 119 TGAFLKSRKAVYENDIKVPEHNLIPWPLFHVASKGKMLAETLLEY 178

Qy 175 ALKDYDVRNTVHPGYIKTPL-VDDLPGEAEAMSQRTKTPMGHEPNDAIYCVLASN 233

Db 179 APK-GIVNNNPGAINPINAKEFADEPQRADVESMPGMGTYGPEEEIAAV-AWLLAS 235

Qy 234 ESKPATGSEFVVDGGYT 250

Db 236 EASTVTGTTLFADGMT 252

RESULT 13

ID DHG_BAC5 STANDARD; PRT; 261 AA.

ID DHG_BAC6 STANDARD; PRT; 261 AA.

AC P12310; P94430; 01-OCT-1989 (Rel. 12, Created)

DT 01-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Glucose 1-dehydrogenase (EC 1.1.1.47).

GN GDH

OS Bacterium; Firmicutes; Bacilli; Clostridia group;

OC Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

NCBI_TaxID=1423;

RN SEQUENCE FROM N.A.

RP MEDLINE-86166021; PubMed-3082854;

RA Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.; "Characterization of the developmentally regulated *Bacillus subtilis* glucose dehydrogenase gene." J. Bacteriol. 166:238-243(1986).

GN	GDHIV.	DE	Glucose 1-dehydrogenase II (EC 1.1.1.47) (GLCDH-II)
OS	Bacillus megalaterium.	GN	GHII.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;	OS	Bacillus megalaterium.
OC	Bacillus/Staphylococcus group; Bacillus.	OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OX	NCBI_TaxID=1404;	OC	Bacillus/Staphylococcus group; Bacillus.
RN	[1]	OX	NCBI_TaxID=1404;
RP	SEQUENCE FROM N.A.	RN	[1]
RC	STRAIN=IAM 1030;	RP	SEQUENCE FROM N.A.
RC	MEDLINE=92332436; PubMed=1629157;	RC	SPRAIN=IAM 1030;
RA	Nagao T.; Mitamura T.; Wang X.H.; Negoro S.; Yomo T.; Urabe I.; Okada H.; RT	RA	Mitamura T.; Ebora R.V.; Nakai T.; Makino Y.; Negoro S.; Urabe I.; Okada H.; RT
RA	"Cloning, nucleotide sequences, and enzymatic properties of glucose dehydrogenase isozymes from <i>Bacillus megalaterium</i> IAM1030."	RT	isozyme genes of glucose dehydrogenase from <i>Bacillus megalaterium</i> IAM1030."
RL	J. Bacteriol. 174:5013-5020(1992).	RL	J. Ferment. Bioeng. 70:363-369(1990).
CC	-I- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)= D-glucono-1,5-lactone + NAD(P)H.	CC	-I- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+)= D-glucono-1,5-lactone + NAD(P)H.
CC	-I- SUBUNIT: HOMOTETRAMER.	CC	-I- SUBUNIT: HOMOTETRAMER.
CC	-I- MISCELLANEOUS: PREFERENCES NADP TO NAD.	CC	-I- MISCELLANEOUS: PREFERENCES NADP TO NAD.
CC	-I- THERMOSTABILITY.	CC	-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC	-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	CC	-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC	(EMBL; D10626; BAA01476.1; -.	DR	EMBL; D90044; BAA14100.1; -.
CC	DR	DR	HSSP; P50162; IASL.
CC	DR	DR	InterPro; IPR002198; ADH_short.
CC	DR	DR	Pfam; PF00106; adh_short; 1.
CC	DR	DR	PRINTS; PRO0080; SDRFAMILY.
CC	DR	DR	PROSITE; PS00061; ADH_SHORT; 1.
CC	DR	FT	NE_BIND 11 35 NADP (BY SIMILARITY).
CC	DR	FT	ACT_SITE 158 158 BY SIMILARITY.
CC	DR	SQ	SEQUENCE 261 AA; 28251 MW; CEF9AA1425D2999C CRC64;
CC	DR	DR	Query Match 27.6%; Score 355.5; DB 1; Length 261;
CC	DR	DR	Best Local Similarity 31.4%; Pred. No. 5e-22; Mismatches 111; Indels 9; Gaps 4;
CC	DR	DR	Matches 80; Conservative 55; Mismatches 100; Indels 29; Gaps 6;
CC	DR	DR	Qy 1 MSNRLLDGKVAVITGGPGLIGIAATKVFEGAKVMT-----DRHSDFGEKAAKSV 51
CC	DR	DR	Db 1 MYTDLKDVKVVYVTGGSGSLGRAMAVRGQEQQSKVYVNRSEEEALEVKKEEAG-GQ 58
CC	DR	DR	Qy 52 GTPDQIQQFDQHSDDEGWTFLDATEKAFPVSTLYNNAGIAVRSVEETTAEMRKULL 111
CC	DR	DR	Db 61 -----IVQSDVTKKEEDVVLVQVPAIKEGTLDMINNAGENPVPSHEISLDWNWKVI 113
CC	DR	DR	Qy 112 AVNLDDGYFFGTRGIORMKNGKGLAGASTINNSSIEGFVGDPSLGAYASKGAVRIMSKAA 171
CC	DR	DR	Db 114 DYNLTAFLGSLSEAIXYFVEDIKGNVNHSSVHENIPWPFLVHAAASKGCKMLTETLA 173
CC	DR	DR	Qy 172 LDCALDYDVRYNTVHPGYIKTPL----VDDLPGA-EAMSQRKTPMGHIGEPNDIA 225
CC	DR	DR	Db 174 LEYAPK-GIVRNNTCPGAMNTPINAKFADPVQARDVSM----IPMSYTGKEEEVA 226
CC	DR	DR	Qy 226 ICYLASNESEPATGSBFFVVOGYT 250
CC	DR	DR	Db 227 VAAFLASSQASYVTGITLEADGGMT 251
CC	DR	DR	Qy 236 KPATGSEFFVVDGGYT 250
CC	DR	DR	Db 237 SYVTGITLEADGGMT 251
CC	DR	DR	Search completed: October 30, 2002, 15:45:26
CC	DR	DR	Job time : 14 secs

RESULT 15

DIG2_BACME ID DHG2_BACME STANDARD PRT 261 AA.
 AC P19483; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - Protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 27 Seconds

(without alignments)

1614.619 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 1290

Sequence: 1 MSRLDGKVAITTGGTIGIG.....NESKFATGSEFVYDGGYTAQ 252

Scoring table: BLOSUM62

Gapext 0.5

searched: 562222 seqs, 12994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:^{*}1: sp_archaea:^{*}2: sp_bacteria:^{*}3: sp_fungi:^{*}

4: sp_human:

5: sp_invertebrate:^{*}6: sp_mammal:^{*}7: sp_minhc:^{*}8: sp_organelle:^{*}9: sp_phage:^{*}10: sp_plant:^{*}11: sp_rabbit:^{*}12: sp_virus:^{*}13: sp_vertebrate:^{*}14: sp_unclassified:^{*}15: sp_rvirus:^{*}16: sp_bacteriap:^{*}17: sp_archeap:^{*}

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	470	36.4	261	16	Q9ABI1	Q9abil caulobacter
2	452.5	35.1	250	2	Q937L4	Q93714 comamonas t
3	438	34.0	254	2	Q9RK49	Q9k4g9 streptomyce
4	411	31.9	251	2	Q9RNK5	Q9rnk5 zymomonas m
5	411	31.9	254	2	Q92587	Q92587 comamonas t
6	395.5	30.7	256	2	Q93QG5	Q93qg5 brevibacter
7	391	30.3	249	2	Q56841	Q56841 xanthobacte
8	386.5	30.0	247	2	Q93RM0	Q93rm0 acinetobact
9	386.5	30.0	251	2	Q9E7E0	Q9f7e0 acinetobact
10	378.5	29.3	258	2	Q9JN17	Q9jn17 agrobacteri
11	374.5	29.2	255	16	Q98ENO	Q98eno rhizobium 1
12	374.5	29.0	248	16	Q116B0	Q316B0 bacillus su
13	374.5	29.0	250	16	Q98C63	Q98c63 rhizobium 1
14	373	28.9	249	2	Q9LBG5	Q9lb5 geobacillus
15	372.5	28.9	253	16	Q930L7	Q930l7 rhizobium m
16	370	28.7	246	2	Q9EX74	Q9ex74 rhodococcus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	Q9ABI1	ID	Q9ABI1	PRELIMINARY:	PRF:	261 AA.
		AC	Q9ABI1;			
		DT	01-JUN-2001	(TREMBLrel. 17, Created)		
		DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
		DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
		DE	2,5-DICHLORO-2,5-CYCLOCHEXADIENE-1,4-DIOL DEHYDROGENASE.			
		GN	CC0246.			
		OS	Caulobacter crescentus.			
		OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;			
		OC	Caulobacter.			
		RN	NCBI_TaxID=9394;			
		RN	[1]			
		RP	SEQUENCE FROM N.A.			
		RC	STRAIN=ATCC 19089 / CB15.			
		RX	MEDLINE=2117698; Published=11259647;			
		RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Phadnis C., Gwin M.L., Haft D.H., DeBoy R.T., Dodson R.J., Durkin A.S., Smit J., Craven M.B., Khouri H., Shetty J., Ermolaeva M., White O., Kolonay J.F., Utterback T., Tran K., Wolf A., Yamatievev C.M., Prok Natl Acad Sci U.S.A. 98:4156-4161 (2001).			
		RA	~1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.			
		CC	EMBL; AE005698; AAK22233.1; -.			
		CC	TIGR; CC0246; -.			
		DR	InterPro; IPR002198; ADH_short.			
		DR	PFam; PF00106; adh_short; 1.			
		DR	PRINTS; PR0080; SDREPAIR.			
		DR	PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.			
		KW	Complete proteome; Oxidoreductase.			
		SQ	SEQUENCE 261 AA.; CE011D872D4EBA6D CRC64;			

Query Match 36.4%; Score 470; DB 16; Length 261;

ALIGNMENTS

Best Local Similarity 40.7%; Pred. No. 7.7e-28; Matches 10; Conservative 46; Mismatches 90; Indels 20; Gaps 6;	Q9k4G9 PRELIMINARY; PRT; 254 AA.
Qy 2 SNRLDGKVAITGGTGLGILAIATKFEVEGAKYMITDRHSVGEKAASKSGVGTGDPDQIQQH- 58	ID Q9k4G9 AC Q9k4G9; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Db 5 TGRVAGKRAFKITGQGLAAAGRMLAKEGAKYAL---ADINLAGOAVA--DEINAAH 58	DE PUTATIVE OXIDOREDUCTASE. GN SC066_06. OS Streptomyces coelicolor. OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae; Actinomycetales; Streptomycineae; Streptomycetes.
Qy 59 ---FPOHDSSDEDGWTKLFDATERAFGPVSTLVNNAGTAVNKSVEETTAEWKRKLLA 112	OX NCBI_TAXID=1902;
Db 59 GAGTAAFAEFLDVTQEDQWTDLEKATAAMGGLSVLVNNAGIGGDGPTESLDLGWLKKVNS 118	RN [1] RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Cerdeno A.M.; Parkhill J., Barrell B.G., Rajandream M.A.; RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. RN [2] RN [3]
Qy 113 VNLDGFFFGTRLGIQRKGKLGASITINMSSTEGFGDPGAYNASKGAVRIMSKSAAI 172	RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Oliver K., Harris D.; RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. RN [2] RN [3]
Db 119 VNVDSVFLGAKHALTHMRAHQPG-SIINLSSLAGLIANGNSPANYNSAAVWLLSKNIAL 177	RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Cerdeno A.M.; Parkhill J., Barrell B.G., Rajandream M.A.; RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. RN [2] RN [3]
Qy 173 DCALKDGYRVRNTYHPGTYKTPVPLVDDLP--GAEAMSQRTK-TPMGHIGEPNDIAVICV 228	RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Cerdeno A.M.; Parkhill J., Barrell B.G., Rajandream M.A.; RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. RN [2] RN [3]
Db 178 YCAKMKLDIIRSNSHIPTDTPGARFGEAFAKLARQVPLGRIGEPTDIANAVL 237	RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Redenbach M., Kieser H. M., Denapante D., Eichner A., Cullum J., RA Kuniishi H., Hopwood D. A.; RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; RT Mol. Microbiol. 21:77-96 (1996). RL Mol. Microbiol. 21:77-96 (1996). CC - I SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY. CC (SDR) FAMILY. DR EMBL; AL15692; CAB94073.1; -. DR HSSP; P19992; 1HDC. DR InterPro; IPR002198; ADH_short. DR PRINTS; PRO0080; SDRFamily. DR PROSITE; PS00061; ADH_SHORT. KW Oxidoreductase. SQ SEQUENCE 254 AA; 26132 MW; A372F691F1B88672 CRC64;
Qy 229 YLSNESKPATGSEFVVDGGYTA 251	Query Match 34.0%; Score 438; DB 2; Length 254; Best Local Similarity 40.7%; Pred. No. 1.9e-17; Indels 6; Gaps 4;
Db 238 YLASDESFRMTGAEIKVKGIGISA 260	Mismatches 100; Conservative 40; SQ SEQUENCE 254 AA; 26132 MW; A372F691F1B88672 CRC64;
RESULT 2	
Q937L4 PRELIMINARY; PRT; 250 AA.	Q937L4 PRELIMINARY; PRT; 250 AA.
AC Q937L4; DT 01-DEC-2001 (TREMBLrel. 19, Created)	AC Q937L4; DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLOHEXANOL DEHYDROGENASE (EC 1.1.1.1).	DE Xanthobacter and Rhodococcus via PCR with highly degenerate primers.;"
GN Comamonas testosteroni (Pseudomonas testosteroni).	GN Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
OS Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.	OS Comamonas testosteroni (Pseudomonas testosteroni).
OX NCBI_TAXID=285;	OX NCBI_TAXID=285;
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.
RC STRAIN-NCIMB 9872;	RC STRAIN-NCIMB 9872;
RT Cloning of Baeyer-Villiger monooxygenases from Comamonas, Xanthobacter and Rhodococcus via PCR with highly degenerate primers.;"	RT van Ballen J.B., Fritzsche U., Seeger M., Smits T.H.M., Witholt B.; Xanthobacter and Rhodococcus via PCR with highly degenerate primers.;"
RL EMBL; AJ418060; CAD10799.1; -.	RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR DR	DR DR
KW Oxidoreductase.	KW Oxidoreductase.
SQ SEQUENCE 250 AA; 26626 MW; 7C42C3CBAAEBB859E CRC64;	Qy 5 LDGKVAITGGTGLGILAIATKFEVEGAKVMTDRHSVGEKAASKSGVGTGDPDQIQFFHDS 64 Db 4 LTGKVNLTGGARGLGAEARQAVAGHLVNLNAGISTEPLESESDVHLRKVLDNITGFGVFMKT 61
Query Match 35.1%; Score 452.5; DB 2; Length 250;	
Best Local Similarity 38.8%; Pred. No. 1.5e-26; Indels 5; Gaps 4;	Qy 65 SDEDGNTKLFDATEKAFGPVSTLVNNAGTAVNKSVEETTAEWRKLAIVNLDGVFFCTRL 124 Db 62 TSBEDWSRADPAVTEGALHGVLNNGAISTEPLESESDVHLRKVLDNITGFGVFMKT 121
Matches 97; Conservative 48; Mismatches 100; Indels 5; Gaps 4;	Qy 125 GIORMKKGKGASIIINNSSIEFGVGDPSLGLAYNASKGAVRIMSKSAALCDALKDYDRVN 184 Db 122 VVPALKRAG-GGSIVTNNSAAGLMGLALTAGYASKWGRGLTKIGVWEWGTAA-RRVN 178
SEQUENCE 250 AA; 26626 MW;	Qy 185 TVHPGYIKPLVDDLPAAEAMSQRTKPMGHIGEPNDIAYCVYLASNESKFATGEFV 244 Db 179 SVHPGTYTPTAAV-GIERGEGKYPNPMGRVGEADIAVGAVVFLSDAAKVTVGELA 237
Qy 63 DSSDEDGWTKLFDATEKAFGPVSTLVNNAGTAVNKSVEETTAEWRKLLAIVNLDGVFFGT 122	Qy 245 VDGGYT 250 Db 238 VDGGWT 243
Db 63 DVTNENHWTGAVDFTILAESDRDALVNNACTLTKEPVQDTNEEDRIFENVRSVFLGT 122	RESULT 4
Qy 123 RJGJQRMKKGKGASIIINNSSIEFGVGDPSLGLAYNASKGAVRIMSKSAALCDALKDYDRV 182	Q9RNRK5 ID Q9RNRK5 AC Q9RNRK5; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
Db 123 RAVIEPARKAKGK-IVNVSSTYGLVGAQAAYEASKGARLFLTKACAVY--LAFENIR 179	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Qy 183 VNTVHPGYIKTPVLYD-LPGEEAMSQRTKPMGHIGEPNDIAYCVYLASNESKFATGS 241	
Db 180 VNSVHPGVIATPMTOQILDAQSARALLGPVLLGRAAQPMVSQAVLFYSEASVHG 239	
Qy 242 ERYVDDGTYA 251	
Db 240 ELVVDGSYTA 249	
RESULT 3	

BETA-HYDROXYSTEROID DEHYDROGENASE	
DE	Zymomonas mobilis.
OS	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC	Zymomonas.
OC	NCBI_TaxID=542;
OX	RN [1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ZM4;
RA	Lee H.J., Kang H.S.;
RT	*Sequence analysis of 42F4 fosmid clone of Zymomonas mobilis 2M4 submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL	-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCT
CC	(SDR) FAMILY.
CC	EMBL; AF180145; AAD56922.1; -.
DR	HSSP: P19992; 1HDC.
DR	InterPro: IPR02198; ADH_short.
DR	Pfam: PF00106; adh_short; 1.
DR	PRINTS: PRO0080; SDRFAMILY.
KW	Oxidoreductase.
SEQUENCE	251 AA: 26621 MW: 62DD151CAF07CF6B CRC64:
Qy	Query Match 31.9%; Score 411; DB 2; Length 251;
Best Local Similarity 40.6%; Pred. No. 2, 1e-23;	
Matches 101; Conservative 33; Mismatches 95; Indels 20; C	
Db	5 GGTIGGLIAATKFVEGAKVYMITDRHSIVGEKAAKSVGTPOIOFFQHQHDSDEDGWTKI
Qy	74 FDATEKAFGPYSTLVNNAGI-----AVNKSVETTTAENRKLLAVNLGVFPGTRLGIG
Db	61 AE1PV ----YDVVVVRNAGITGFENGAVAHPEHATLEDFRHRVNLDDGFLGCNYAI
Qy	128 RMKNKGIGASLTINMSSTEGVGDPSLGAYNASKGAVRIMSKAALDKDLYDVRVNTV
Db	117 AMKNGKTG-STINNISRG-SIINNISRG-YGPILAAYASAKA-TRNHSISVALYCAQQWKIRQNII
Qy	188 PGYIKTPVLDDLPGLGABEAMSORTK-----TPMHGICEPNDIAYICYLASNESKEPATGS
Db	176 PAAILTSIWEPMGLGDDDRKRMQALVADPLKRGFLPEVAAVMLASDEATIMTGAI
Qy	243 FVVDGGYT A 251
Db	236 FNIDGGLLA 244
RESULT 5	
ID	Q52587 PRELIMINARY; PRT; 254 AA.
AC	Q52587;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB	BETA-HYDROXYSTEROID DEHYDROGENASE
OS	Comamonas testosteronei (Pseudomonas testosteronei).
CC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonadaceae;
CC	NCBI_TaxID=285;
RN	RN [1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE-ATCC 11996;
RA	Cabreira J.E., Gentil-Raimondi S.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC	-1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCT
CC	(SDR) FAMILY.
DR	U41265; AAA25742.1; -.
DR	HSSP: P19992; 1HDC.
DR	InterPro: IPR02198; ADH_short.
DR	Pfam: PF00106; adh_short; 1.
DR	PRINTS: PRO0080; SDRFAMILY.
DR	PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW	Oxidoreductase.
SEQUENCE	254 AA: 26952 MW: FB66C90B151975DB CRC64:

	Query Match	Similarity	Score	DB	Length	254;
Best Local Matches	31.9%	Score 411; Pred. No. 2.1e-13;	DB 2;			
Conservative Matches	36.8%	Mismatches 48; Indels 102;	DB 3;			
				Indels	8;	Gaps
29Y	1 MNRUDGKVATITGGTGLIGLAIATKVFEGAKYMTIDRHSVDGVTPDQIQOFF 60					
	1 MTRLGKVALVTTGGAGLVEVRLGLGAKAFAFSDNEAGQOLAAELG - ERSMFVY 58					
29D	61 QHDSSDEGWTKLFDATKEAFGPVSTLVNNAGIANKSVDETTAEWRKLAVNLGDGVFF 124					
	: : : : : : : : : : : : :					
29b	59 RHDVSSEADNTLVMAVORRGTLTANVLNVRAGILPGDNETGRLEDESRLKINTESVFI 116					
	: : : : : : : : : : : : :					
29Y	121 GTRLGJORMKNRKGLGASINMSSIEFGVDPGSAGAYNASKGAVRIMSKSAALDCALKDYD 180					
	: : : : : : : : : : : : :					
29b	119 GCQGTAAMKE - TGGSIIINMASVSSWLPLEQYAGSASKAASVSLRAAALSCKQGYA 176					
	: : : : : : : : : : : : :					
29Y	181 VRVNTVHPGVIKTPFLPD - DLP - - GAEAMSQRKTPGMGHPEPDIAVCYVLASNEK 236					
	: : : : : : : : : : : : :					
29b	177 IRVNSLHPDGJYTPMQASLPEKGYSKEMVLDPPKLNRAGRAYMPERIAOLYLFLASDESS 238					
	: : : : : : : : : : : : :					
29Y	237 PATGSEFVVD 246					
	: : : :					
29b	237 VMSGSELHAD 246					
30Y	RESULTS 6					
	993QGS	PRELIMINARY;	PRT;	256 AA.		
	Q93QGS					
	Q93QGS;					
	01-DEC-2001 (TREMBLrel. 19, Created)					
	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
	CYCLOHEXANOL DEHYDROGENASE.					
	CHNA.					
	Brevibacterium sp. HCU.					
	Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;					
	Actinomycetales; Micrococcineae; Brevibacteriaceae; Brevibacterium.					
	NCBI_TaxID=133406;					
	[1]					
	SEQUENCE FROM N.A.					
	STRAIN=HCU;					
	BRZESTOWIAZ P.C., BLASKO M.S., ROUVIERE P.E.;					
	*Identification of Two Gene Clusters Involved in Cyclohexanone in					
	Brevibacterium sp. HCU.;					
	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.					
	EMBL: AF257214; AAKJ3164.1; -					
	SEQUENCE 256 AA; 26518 MW; C483D9F6BD8D1836 CRC64;					
	Query Match Similarity 30.7%; Score 395.5; DB 2; Length 256;					
	Best Local Matches 37.7%; Pred. No. 3.1e-22;					
	Conservative Matches 43; Mismatches 104; Indels 15; Gaps					
30Y	3 NRLDGKVATITGGTGLIGLAIATKVFEGAKYMTIDRHSVDGVTKPMSKAALDCALKDYD 61					
	: : : : : : : : : : : : :					
30b	2 NRLLGKVALVTTGGAGMGRQSEIYASSEGQAQVAVDVNQEGRATAIDARASCGCVANTWK 61					
	: : : : : : : : : : : : :					
30Y	62 HDSSDEGWTKLFDATKEAFGPVSTLVNNAGI - AVNKSVWEETTAEWRKLAVNLGDGVFF 120					
	: : : : : : : : : : : : :					
30b	62 LDVSDSEYEIVVSDIAKRGAINVNNAGITGADKPTHEIDRDLVLSYDKGTYFF 121					
	: : : : : : : : : : : : :					
30Y	121 GTRLGJORMKNRKGLGASINMSSIEFGVDPGSAGAYNASKGAVRIMSKSAALDCALKDYD 180					
	: : : : : : : : : : : : :					
30b	122 MTKICIPYKQAG - GGAIYNFASTYGLGSQELPTYHAKGAVVLTQDAV - TYGPSN 178					
	: : : : : : : : : : : : :					
30Y	181 VRVNTVHPGVIKTPFLPD - DLP - - GAEAMSQRKTPGMGHPEPDIAVCYVLASNEK 232					
	: : : : : : : : : : : : :					
30b	179 IRVNAVAPGTILTLVKELGSRGPDGLOSYTKLNG - -AKHPLQRVTPEVAATLFLAS 236					
	: : : : : : : : : : : : :					
30Y	233 NESKFATGSEEFVWDGGYTAQ 252					
	: : : : : : : : : : : : :					
30b	237 EEA8FTGAVLPVGPGYTAQ 256					

Db	65	MKANTAPEDKAAVEFAVSPFGAHLAFNNAIGILGEVN-STEELSIEGHRVIDVNLA	123	Qy	124	LGIQRMKNGKGASITINMSSIEGFYGD--PSLGAYNAVKAVRIMSKSAALDCALKDYDV	181
Qy	118	VFFGTRUGIQRMKNGKGASITINMSSIEGFYGDPSLGAIVNRSKGAVRIMSKSAALDCALK	177	Db	130	AAIPYARREGGRGA-IVNVGSMGIVSNIPQNQVATNSKAAVHMTRKSLSAELLD-NI	186
Db	124	VFYSMHVEPAAILAAG-GGAIVNTASTIAGLIGIONISGTYAHHGTGLIKAALEYA--	180	Qy	182	RVNTYHPGYIKTPLYDLPAAEAMSRKTPMGHIGEPNDIAYICVYLASENE	234
Qy	178	DYDVRNTVHGGYIKPLVDDLPGAAEAMSRKTPMGHIGEPNDIAYICVYLASENF	237	Db	187	RVNAYAPGYIDDM-SRGGMVHPVRSPIWLEMTPMRKGDEIAITFLASEA	240
Db	181	DKGIRLNSVHGGYIKPLIAEEAEAMVKLH---PIGRLGQPEEVQAQVVAFLSSDASF	236	Qy	235	SKEATGSEFVYDGGTAQ	252
Qy	238	ATGSEFVYDGGTAQ	252	Db	241	SSYVTDILVVDGGTTT	258
Db	237	VTGSQIVWDGATSK	251				
		RESULT 11					
		Q98ENO					
		ID Q98ENO					
		PRELIMINARY;					
		PRT; 258 AA.					
		AC Q9JN17;					
		AC 09JN17;					
		DT 01-OCT-2000 (TREMBLrel. 15, Created)					
		DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)					
		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
		DE YHG.					
		GN Rhizobium loti (Mesorhizobium loti)					
		OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;					
		OC Phyllobacteriaceae; Mesorhizobium;					
		OC NCBI_TaxID=381;					
		RN [1]					
		RP SEQUENCE FROM N.A.					
		RC STRAIN=MATE303099;					
		RR MDDLINE=21082930; PubMed=11214968;					
		RA RX RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,					
		RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,					
		RA Kishida Y., Kiyokawa C., Kohara M., Matsuno A.,					
		RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,					
		RA Takeuchi C., Yamada M., Tabata S.;					
		RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium					
		RT Mesorhizobium loti";					
		RL DNA Res. 7:331-338(2000).					
		DR EMBL; AP003003; BAB5088.1; -;					
		DR Interpro; IPR002198; ADH_short.					
		DR Pfam; PF00106; adh_short; 1.					
		DR PRINTS; PRO0080; SDRFAMILY.					
		KW Complete proteome.					
		SQ SEQUENCE . 255 AA; 26441 MW; 7EA89BB4.6810117 CRC64;					
		Query Match 29.2%; Score 376.5; DB 16; Length 255;					
		Best Local Similarity 38.3%; Pred. No. 8.4e-21;					
		Matches 101; Conservative 37; Mismatches 103; Indels 23; Gaps 7;					
		Qy 1 MSNRLLDGKVATITGGTIGIGLIAITAKFVGKAVMTDRHSVGEKAKSVGTPDOL-QF 59					
		Db 1 MGRLAGKVALISGATGMGAASELFAAVAKVLDNRGEAAAATAIRARGVAAEH 60					
		Qy 60 FQHDSSDE-DGWTKLEDATEKAFGVSTLVNNAGAVANKSVETTAEWRKLNLNDGV 118					
		Db 61 FVADYSDEAQYQAAVTKGATEK-LGPVTVLPNHAGTVKPFLETYQENDWLHATVNRSM 119					
		Qy 119 FFGTRJLQRMKNGKGASITINMSSIEGFYGDPSLGAIVNASKGAVRIMSKSAALDKD 178					
		Db 120 FLMPRAVLPGMIAAG-GGSIVCSTSSTVATPMEVLYPTDKGCHMFARIAVE-FRD 176					
		Qy 179 YDVRNTVHGGYIKTP- LVDLPGAEAMSORTKTPMGHIGEPNDIAYIC 227					
		Db 177 RNIRNCVACGFGIRDPGLREVADLQLRGVYDVSAAQO---GRIGEPEEVAKAA 230					
		Qy 228 VYLASNESKRATGSSFEVWDGTYA 251					
		Db 231 LYLASDESSPVNGAHLFVFDNGFTA 254					
		RESULT 12					
		031680 ID O31680 PRELIMINARY; PRT; 248 AA.					

AC	O31680:	DR	01-JAN-1998 (TREMBLrel. 05, Created)	Db	121 KALSLFPDK - VGSIIITVGSTAGSIGNPAPSVYGASKAALRALVRNWILD - LKGTEIRV 176
		DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	Qy	184 NTVHPGYIKTPVLVDLPG - AEEAM-SQRTKTPMCHIGEPNDIAYCVLASNEKFATG 240
		DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	Db	177 NVVSPGILTPAYDEFGDALEEVLENSRTVPAKGVTPEEVANASFLASDESYLTG 236
DE	YKV0 PROTEIN.				
GN	Bacillus subtilis.				
OS	Bacteria; Firmicutes; Bacillales; Closstridium group;				
OC	Bacillales;Staphylococcus group; Bacillus.				
OC	NCBI_TaxID=1422;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=168;				
RX	MEDLINE=BB044033; PubMed=9384377;				
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Bertero M.G., Bassieres P., Bolotin A., Borchert S., Borriss R., Bourquier L., Braus A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton J.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulier D., Fritz C., Fujita M., Fujita Y., Fumagalli A., Galleron N., Ghin S.Y., Glaser P., Goffeau A., Goliath E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haileich J., Harbeck J., Hilbert H., Hollsappel S., Hosono S., Hullu M.E., Itaya M., Jones L., Juris B., Karamata D., Kasahara Y., Klaerr-Banchard M., Klein C., Kobayashi Y., Koetter P., Koningschein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Ono T., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadie Y., Sato T., Scanlan E., Schleicher S., Schooterter R., Scoffone P., Sekiguchi J., Sekowska A., Seror S.P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takahashi H., Takemoto K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandembol F., Vannierotti A., Vilar A., Wambutt R., Wedler E., Weltzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yoshida K., Yoshikawa H., Zumstein E., Yoshikawa H., Danchin A.; The complete genome sequence of the gram-positive bacterium subtilis.]; Nature 390:249-256(1997).	Score 29.0%; Best Local Similarity 37.5%; Pred. No. 1.2e-20; Matches 93; SEQUENCE FROM N.A.	RL	29.0%; Score 374.5; DB 16; Length 250; Best Local Similarity 37.1%; Pred. No. 1.2e-20; Matches 93; SEQUENCE FROM N.A.	
RP	STRAIN=168;				
RC	Kunst F., Ogasawara N., Yoshikawa H., Danchin A.; Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases (ISDR) FAMILY.	Score 29.0%; Best Local Similarity 37.5%; Pred. No. 1.e-20; Matches 93; SEQUENCE FROM N.A.	RL	29.0%; Score 374.5; DB 16; Length 248; Best Local Similarity 37.1%; Pred. No. 1.2e-20; Matches 93; SEQUENCE FROM N.A.	
CC	ENSP; P47227; 1BDR.				
CC	InterPro; IPR02198; ADH_short.				
CC	Complete proteome; Oxidoreductase.				
CC	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
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DR	EACA490C1239524D CRC64;				
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DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;				
DR	InterPro; IPR02198; ADH_short.				
DR	Complete proteome; Oxidoreductase.				
DR	SEQUENCE 248 AA; 26245 MW;				
DR	EACA490C1239524D CRC64;		</		

DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RT	"Nucleotide sequence and predicted functions of the entire
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	RT	Sinorhizobium meliloti plasmid."
DE	SHORT CHAIN ALCOHOL DEHYDROGENASE.	RL	Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
GN	BT-ADH.	DR	EUBL; AE007211; AAK6436.1;
OS	Geobacillus thermoleovorans.	KW	Plasmid; Hypothetical protein; Complete proteome.
OC	Bacteria; Firmicutes; Bacilli; Clostridium group;	SQ	SEQUENCE 253 AA; 26136 MW; CDB021316BA99EEF CRC64;
OC	Bacillus/Staphylococcus group; Geobacillus.		
OX	NCBI_TAXID=33941;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=B23;		
RA	Moriakawa M., Kanaya S., Kato T.;		
RA	"Short chain alcohol dehydrogenase of <i>Bacillus thermoleovorans</i> B23.";		
RT	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.		
RL	- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES		
CC	(SDR) FAMILY:		
CC	EMBL; AB00809; BAA94092.1; -.		
DR	HSSP; P19992; 1HDG.		
DR	InterPro: IPR002198; ADH_short.		
DR	InterPro: IPR00205; NAD_binding.		
DR	PRINTS: PR00080; SDRFAMILY.		
DR	PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.		
DR	Oxidoreductase.		
DR	PS00061; ADH_SHORT; UNKNOWN_1.		
KW	SEQUENCE 249 AA; 27197 MW; 072B0DF7C6CEA31 CRC64;		
SO			
Query Match	28.9%; Score 373; DB 2; Length 249;		
Best Local Similarity	34.5%; Pred. No. 1.5e-20;		
Matches	90; Conservative		
Qy	5 LDGRVATIGGTGIGLIAATKFVEGAKVMTDRHSVDGEKAKSVGTPDQIQFFQHDS 64		
Db	3 IEQKTAIVTGANGIGKRAFRAKQANVITDRIQNGEFAA-----QLQ-----50		
Qy	65 SDEDGWTKLFEDATE-----KAGPVSTLYNNAGIAYVNKSVEETTAEWRK 109		
Db	51 --SDGFEAIFVAADVVKYDDIEFVQDRAAGRGGRIDYLNNAGVSRMKSPELTVEWDD 108		
Qy	110 LLAVNLQGVFGTRGLQMRMKNGLNASIIINMSIEFGVGDLSGAYNASKGAVRIMSKS 169		
Db	109 VLSNTNLSAFAFASREAAKYMRRNAKGSAIVINASTRALMSEENSEAAYASKGVLVAMTHA 168		
Qy	170 AALDCALKDYDVRNTVHPGYIKPLVDDLGAEAMSQTATPMGHGEPENDIATCVY 229		
Db	169 LAVSFA--DDRIRVNCISPWIEFTGQWLIDRQDID----HRQPHAGRVKPDIIARACLY 221		
Qy	230 LASNESFVDFVYDGGY 250		
Db	222 LCDDEENDFTGVNLVIDGMM 242		
Search completed: October 30, 2002, 15:46:02			
Job time : 31 secs			
RESULT 15			
ID	Q930L7	PRELIMINARY;	
AC	Q930L7;	PRT;	253 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	PUTATIVE.		
GN	SM0329.		
OS	Rhizobium meliloti (Sinorhizobium meliloti).		
OG	Plasmid pSymA (megaplasmid 1).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;		
OC	Rhizobiaceae; Sinorhizobium.		
OX	NCBI_TAXID=382;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=1021;		
RX	MEDLINE-21396509; PubMed=11481432;		
RA	Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,		
RA	Barlow-Hubler F., Bowser L., Capela D., Galibert F., Gozzy J.,		
RA	Gurjal M., Hong A., Huizar L., Hyman D.W., Kahn M.L.,		
RA	Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Weils D.H.,		
RA	Yeh K.-C., Davis R.W., Fedderspiel N.A., Long S.R.,		